

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 35.1493 Seconds  
(without alignments)  
120.578 Million cell updates/sec

Title: US-09-641-802-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	81	100.0	15	4	AAB72506	Aab72506 Colostrin
2	81	100.0	15	4	AAB59312	Aab59312 Ewe colos
3	81	100.0	15	4	AAB72252	Aab72252 Colostrin
4	81	100.0	15	4	AAB72538	Aab72538 Colostrin
5	81	100.0	15	5	AAO14583	Aao14583 Neural ce
6	81	100.0	15	5	AAM51042	Aam51042 Colostrin
7	81	100.0	15	5	AAE20234	Aae20234 Colostrin
8	81	100.0	16	4	AAB59343	Aab59343 Ewe colos
9	38	46.9	14	2	AAR06249	Aar06249 Antigenic

10	38	46.9	18	2	AAW47567	Aaw47567	Exendin a
11	38	46.9	18	2	AAW47571	Aaw47571	Exendin a
12	38	46.9	18	2	AAW47577	Aaw47577	Exendin a
13	38	46.9	18	2	AAW47550	Aaw47550	Exendin a
14	38	46.9	18	2	AAAY03738	Aay03738	Exendin a
15	38	46.9	18	2	AAAY03721	Aay03721	Exendin a
16	38	46.9	18	3	AAB52880	Aab52880	Extendin
17	38	46.9	18	3	AAB52886	Aab52886	Extendin
18	38	46.9	18	3	AAB52876	Aab52876	Extendin
19	38	46.9	18	3	AAB52885	Aab52885	Extendin
20	37	45.7	15	5	ABG72860	Abg72860	Human rib
21	37	45.7	18	2	AAW05469	Aaw05469	SH3-bindi
22	37	45.7	18	2	AAW37677	Aaw37677	PPPPY mot
23	37	45.7	18	2	AAW38909	Aaw38909	Peptide r
24	37	45.7	18	2	AAW47562	Aaw47562	Exendin a
25	37	45.7	18	2	AAAY03733	Aay03733	Exendin a
26	37	45.7	18	7	ADB49303	Adb49303	Novel WW
27	36	44.4	10	2	AAR07284	Aar07284	Smooth mu
28	36	44.4	14	4	AAG79174	Aag79174	Peptide d
29	36	44.4	15	4	AAG79166	Aag79166	Synthetic
30	36	44.4	18	2	AAW47569	Aaw47569	Exendin a
31	36	44.4	18	2	AAW47552	Aaw47552	Exendin a
32	36	44.4	18	2	AAW47564	Aaw47564	Exendin a
33	36	44.4	18	2	AAAY03740	Aay03740	Exendin a
34	36	44.4	18	2	AAAY03723	Aay03723	Exendin a
35	36	44.4	18	2	AAAY03742	Aay03742	Exendin a
36	36	44.4	18	2	AAAY03735	Aay03735	Exendin a
37	36	44.4	18	3	AAB52878	Aab52878	Extendin
38	36	44.4	18	3	AAB52873	Aab52873	Extendin
39	35	43.2	10	2	AAW47943	Aaw47943	AE101 ana
40	35	43.2	10	4	AAU09138	Aau09138	Ena/VASP
41	35	43.2	12	2	AAW48084	Aaw48084	AE101 ser
42	35	43.2	13	2	AAW38053	Aaw38053	Peptide r
43	35	43.2	13	7	ADB49201	Adb49201	Biotinyla
44	35	43.2	15	1	AAP10189	Aap10189	Sequence
45	35	43.2	15	1	AAP70999	Aap70999	Sequence
46	35	43.2	15	1	AAP80033	Aap80033	Beta-huma
47	35	43.2	15	1	AAP91840	Aap91840	Analogue
48	35	43.2	15	2	AAW39024	Aaw39024	Peptide r
49	35	43.2	15	2	AAW38952	Aaw38952	Peptide r
50	35	43.2	15	2	AAW37268	Aaw37268	Peptide d
51	35	43.2	15	2	AAW69452	Aaw69452	HCG antig
52	35	43.2	15	2	AAW93437	Aaw93437	Human hCG
53	35	43.2	15	3	AAAY87482	Aay87482	Human cho
54	35	43.2	15	3	AAB20559	Aab20559	Human cho
55	35	43.2	15	4	AAU01142	Aau01142	Structure
56	35	43.2	15	4	AAB48388	Aab48388	Human cho
57	35	43.2	15	4	AAU02840	Aau02840	Human Cho
58	35	43.2	15	4	AAB04124	Aab04124	Peptide f
59	35	43.2	16	2	AAW47923	Aaw47923	Mammalian
60	35	43.2	16	4	AAB73469	Aab73469	Mammalian
61	35	43.2	17	6	ABP83411	Abp83411	G protein
62	34	42.0	9	2	AAW47926	Aaw47926	Human MHC
63	34	42.0	9	4	AAU09144	Aau09144	Ena/VASP
64	34	42.0	10	2	AAW47942	Aaw47942	AE101 ana
65	34	42.0	13	2	AAW38008	Aaw38008	WW domain
66	34	42.0	14	4	AAB83035	Aab83035	Human Sma

67	34	42.0	15	2	AAR02172	Aar02172	Peptide w
68	34	42.0	15	2	AAW38059	Aaw38059	PPPPY mot
69	34	42.0	15	2	AAW39006	Aaw39006	Peptide r
70	34	42.0	15	2	AAW38942	Aaw38942	Peptide r
71	34	42.0	15	2	AAW25358	Aaw25358	Abl SH3 d
72	34	42.0	15	5	ABP59535	Abp59535	Human rib
73	34	42.0	15	7	ADB49249	Adb49249	Biotinyln
74	34	42.0	16	2	AAR78284	Aar78284	GnRH immu
75	34	42.0	16	2	AAW82834	Aaw82834	Mutated P
76	34	42.0	16	2	AAW82832	Aaw82832	PY motif
77	34	42.0	16	3	AAY65944	Aay65944	MUC1 muta
78	34	42.0	16	5	AAG66086	Aag66086	Amino aci
79	34	42.0	17	2	AAW83313	Aaw83313	LRP5 prot
80	33	40.7	7	4	AAB72512	Aab72512	Colostrin
81	33	40.7	7	4	AAB59315	Aab59315	Ewe colos
82	33	40.7	7	4	AAB72259	Aab72259	Colostrin
83	33	40.7	7	4	AAB72544	Aab72544	Colostrin
84	33	40.7	7	5	AAO14590	Aao14590	Neural ce
85	33	40.7	7	5	AAM51048	Aam51048	Colostrin
86	33	40.7	7	5	AAE20241	Aae20241	Colostrin
87	33	40.7	9	6	ABR28254	Abr28254	Human can
88	33	40.7	9	6	ABR28248	Abr28248	Human can
89	33	40.7	9	6	ABR28437	Abr28437	Human can
90	33	40.7	9	6	ABR27236	Abr27236	Human can
91	33	40.7	10	6	ABR28537	Abr28537	Human can
92	33	40.7	10	6	ABR28354	Abr28354	Human can
93	33	40.7	10	6	ABR27336	Abr27336	Human can
94	33	40.7	10	6	ABR28332	Abr28332	Human can
95	33	40.7	10	6	ABR27737	Abr27737	Human can
96	33	40.7	10	6	ABR27891	Abr27891	Human can
97	33	40.7	10	7	ADC71020	Adc71020	HLA motif
98	33	40.7	10	7	ADC70961	Adc70961	HLA motif
99	33	40.7	10	7	ADC71147	Adc71147	HLA motif
100	33	40.7	11	5	ABB78448	Abb78448	Gum arabi

# ALIGNMENTS

## RESULT 1

AAB72506

ID AAB72506 standard; peptide; 15 AA.

XX

AC AAB72506;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #7.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.  
 XX  
 PR 17-AUG-1999; 99US-0149310P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations.  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
 |||||  
 Db 1 VLEMKFPPPPQETVT 15

# RESULT 2

AAB59312

ID AAB59312 standard; peptide; 15 AA.

XX

AC AAB59312;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment A-3.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.



XX  
PA (REGE-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA;  
XX  
DR WPI; 2001-071058/08.  
XX  
PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.  
XX  
PS Claim 7; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
|||||  
Db 1 VLEMKFPPPPQETVT 15

RESULT 3  
AAB72252

ID AAB72252 standard; peptide; 15 AA.  
XX  
AC AAB72252;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 7.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
PN WO200111937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US022818.  
XX

PR 17-AUG-1999; 99US-0149311P.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX

DR WPI; 2001-202804/20.

XX

PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
CC have immune response modulatory activity, and are capable of inducing  
CC cytokines. Colostrinin and its derived peptides are useful for inducing  
CC cytokine production, for modulating an immunological response and for  
CC inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15

|||||||

Db 1 VLEMKFPPPPQETVT 15

#### RESULT 4

AAB72538

ID AAB72538 standard; peptide; 15 AA.

XX

AC AAB72538;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #7.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

PD 22-FEB-2001.

XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
 |||||  
 Db 1 VLEMKFPPPPQETVT 15

# RESULT 5

AAO14583

ID AAO14583 standard; peptide; 15 AA.

XX

AC AAO14583;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 7.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.  
 XX  
 PR 17-AUG-2000; 2000WO-US022777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
 |||||  
 Db 1 VLEMKFPPPPQETVT 15

# RESULT 6

AAM51042

ID AAM51042 standard; peptide; 15 AA.

XX

AC AAM51042;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022775.  
 XX  
 PR 17-AUG-2000; 2000WO-US022775.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2002-269150/31.  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of blood  
 PT cell regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide that is  
 CC preferred for use as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. Methods are claimed for:  
 CC inducing a cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ or an  
 CC organism, and the cell is mammalian, including human; modulating an  
 CC immune response in a cell by contact with the immunological regulator  
 CC under conditions effective to induce a cytokine; modulating an immune  
 CC response in a patient by administering an immunological regulator under  
 CC conditions effective to induce a cytokine, where the immunological  
 CC regulator is administered topically or as part of a dietary supplement,  
 CC and where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation by  
 CC contacting blood cells with a blood cell regulator, where the blood cells  
 CC are present in a cell culture or an organism, are mammalian or human, and  
 CC where the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A claimed  
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
 CC active agent such as the present peptide. Cytokines induced by this  
 CC peptide in human leucocyte cultures include interferon-gamma, tumour  
 CC necrosis factor-alpha, interleukin-4, interleukin-6 and interleukin-10  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
 |||||  
 Db 1 VLEMKFPPPPQETVT 15

RESULT 7  
 AAE20234  
 ID AAE20234 standard; peptide; 15 AA.  
 XX

AC AAE20234;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #7.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnerary.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022776.  
 XX  
 PR 17-AUG-2000; 2000WO-US022776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2002-269151/31.  
 XX  
 PT Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog.  
 XX  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress level  
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
 CC organ, or organism; or for treating oxidative damage to the skin of a  
 CC patient e.g. animal or human; to modulate oxidative stress during/ after  
 CC a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
|||||||  
Db 1 VLEMKFPPPPQETVT 15

RESULT 8

AAB59343

ID AAB59343 standard; peptide; 16 AA.

XX

AC AAB59343;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #3.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.9e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
|||||||  
Db 2 VLEMKFPPPPQETVT 16

RESULT 9

AAR06249

ID AAR06249 standard; protein; 14 AA.

XX

AC AAR06249;

XX

DT 09-JAN-2003 (revised)

DT 07-DEC-1990 (first entry)

XX

DE Antigenic peptide fragment selected from the 12 N-terminal AAs of  
DE heptadecagastrin (G17).

XX

KW Gastrin; tumours; peptic ulcers; diptheria toxoid; tetanus toxin.

XX

OS Unidentified.

XX

PN EP380230-A.

XX

PD 01-AUG-1990.

XX

PF 17-JAN-1990; 90EP-00300456.

XX

PR 24-JAN-1989; 89US-00301353.

PR 12-MAY-1989; 89US-00351193.

XX

PA (APHT-) APHTON CORP.

XX

PI Gevas PC, Grimes S, Karr SL, Littenberg RL;

XX

DR WPI; 1990-233029/31.

XX

PT Immunogens against gastrin peptide(s) - used to induce antibodies that  
PT specifically neutralise single form of gastrin, G17 or G34.

XX

PS Claim 8; Page 19; 32pp; English.

XX

CC Antigenic fragments may be attached to an immunogenic carrier and used to  
CC raise Abs to a specific single form of Gastrin ie. G17 or G34. Peptide  
CC fragments capable of binding to these Abs are useful in neutralising anti  
CC -gastrin Abs in vivo. (Updated on 09-JAN-2003 to add missing OS field.)

XX

SQ Sequence 14 AA;

Query Match 46.9%; Score 38; DB 2; Length 14;  
Best Local Similarity 70.0%; Pred. No. 77;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11



Db                    || | |||:
                      5 LEEKRPPPPK 14

RESULT 10

AAW47567

ID    AAW47567 standard; peptide; 18 AA.

XX

AC    AAW47567;

XX

DT    03-JUL-1998    (first entry)

XX

DE    Exendin agonist (18).

XX

KW    Exendin agonist; gastric motility; gastric emptying; treatment; spasm;

KW    postprandial dumping syndrome; postprandial hyperglycaemia;

KW    type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;

KW    Gila monster venom.

XX

OS    Synthetic.

XX

FH    Key                    Location/Qualifiers

FT    Modified-site        18

FT                        /note= "amidated"

XX

PN    WO9805351-A1.

XX

PD    12-FEB-1998.

XX

PF    08-AUG-1997;        97WO-US014199.

XX

PR    08-AUG-1996;        96US-00694954.

XX

PA    (AMYL-) AMYLIN PHARM INC.

XX

PI    Young AA,    Gedulin B,    Beeley NRA,    Prickett KS;

XX

DR    WPI; 1998-145351/13.

XX

PT    Regulating gastrointestinal motility using exendins or their agonists -

PT    for treating spasm, diabetic postprandial hyperglycaemia, impaired

PT    glucose tolerance etc., also in diagnostic investigations.

XX

PS    Example 21; Fig 8; 70pp; English.

XX

CC    The present sequence is an exendin agonist, which reduces gastric

CC    motility and delays gastric emptying. It can be used to treat spasm

CC    (where associated with acute diverticulitis or disorders of the biliary

CC    tract or sphincter of Oddi), postprandial dumping syndrome and

CC    hyperglycaemia (particularly associated with type 2 diabetes), type 1

CC    diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist

CC    is administered to prevent stomach contents passing into the intestines,

CC    then the stomach pumped) and obesity. It can also be administered to

CC    subjects undergoing gastrointestinal diagnostic investigation,

CC    particularly radiological or by magnetic resonance imaging. Exendins,

CC    components of Gila monster venom, have some sequence similarity to

CC    glucagon-like peptides (GLP). They are GLP agonists and have been

CC suggested (US5424286) for treatment of diabetes and prevention of  
CC hyperglycaemia  
XX  
SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 99;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10  
:|::||||  
Db 8 LLFVEFPPPP 17

RESULT 11

AAW47571

ID AAW47571 standard; peptide; 18 AA.

XX

AC AAW47571;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (22).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;

KW postprandial dumping syndrome; postprandial hyperglycaemia;

KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;

KW Gila monster venom.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "amidated"

XX

PN WO9805351-A1.

XX

PD 12-FEB-1998.

XX

PF 08-AUG-1997; 97WO-US014199.

XX

PR 08-AUG-1996; 96US-00694954.

XX

PA (AMYL-) AMYLIN PHARM INC.

XX

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX

DR WPI; 1998-145351/13.

XX

PT Regulating gastrointestinal motility using exendins or their agonists -

PT for treating spasm, diabetic postprandial hyperglycaemia, impaired

PT glucose tolerance etc., also in diagnostic investigations.

XX

PS Example 25; Fig 8; 70pp; English.

XX

CC The present sequence is an exendin agonist, which reduces gastric

CC motility and delays gastric emptying. It can be used to treat spasm

CC (where associated with acute diverticulitis or disorders of the biliary  
 CC tract or sphincter of Oddi), postprandial dumping syndrome and  
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
 CC is administered to prevent stomach contents passing into the intestines,  
 CC then the stomach pumped) and obesity. It can also be administered to  
 CC subjects undergoing gastrointestinal diagnostic investigation,  
 CC particularly radiological or by magnetic resonance imaging. Exendins,  
 CC components of Gila monster venom, have some sequence similarity to  
 CC glucagon-like peptides (GLP). They are GLP agonists and have been  
 CC suggested (US5424286) for treatment of diabetes and prevention of  
 CC hyperglycaemia

XX

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;

Best Local Similarity 60.0%; Pred. No. 99;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10

:| ::||||

Db 8 LLFIEFPPPP 17

# RESULT 12

AAW47577

ID AAW47577 standard; peptide; 18 AA.

XX

AC AAW47577;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (28).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;

KW postprandial dumping syndrome; postprandial hyperglycaemia;

KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;

KW Gila monster venom.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 14

FT /label= Hyp

FT Modified-site 15

FT /label= Hyp

FT Modified-site 16

FT /label= Hyp

FT Modified-site 17

FT /label= Hyp

FT Modified-site 18

FT /note= "amidated"

XX

PN WO9805351-A1.

XX

PD 12-FEB-1998.

XX

PF 08-AUG-1997; 97WO-US014199.

XX

PR 08-AUG-1996; 96US-00694954.

XX

PA (AMYL-) AMYLIN PHARM INC.

XX

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX

DR WPI; 1998-145351/13.

XX

PT Regulating gastrointestinal motility using exendins or their agonists -  
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
PT glucose tolerance etc., also in diagnostic investigations.

XX

PS Example 31; Fig 8; 70pp; English.

XX

CC The present sequence is an exendin agonist, which reduces gastric  
CC motility and delays gastric emptying. It can be used to treat spasm  
CC (where associated with acute diverticulitis or disorders of the biliary  
CC tract or sphincter of Oddi), postprandial dumping syndrome and  
CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
CC is administered to prevent stomach contents passing into the intestines,  
CC then the stomach pumped) and obesity. It can also be administered to  
CC subjects undergoing gastrointestinal diagnostic investigation,  
CC particularly radiological or by magnetic resonance imaging. Exendins,  
CC components of Gila monster venom, have some sequence similarity to  
CC glucagon-like peptides (GLP). They are GLP agonists and have been  
CC suggested (US5424286) for treatment of diabetes and prevention of  
CC hyperglycaemia

XX

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;

Best Local Similarity 60.0%; Pred. No. 99;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10

:| ::||||

Db 8 LLFIEFPPPP 17

RESULT 13

AAW47550

ID AAW47550 standard; peptide; 18 AA.

XX

AC AAW47550;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (1).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;  
KW postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;  
KW Gila monster venom.

XX

OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "amidated"  
 XX  
 PN WO9805351-A1.  
 XX  
 PD 12-FEB-1998.  
 XX  
 PF 08-AUG-1997; 97WO-US014199.  
 XX  
 PR 08-AUG-1996; 96US-00694954.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young AA, Gedulin B, Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1998-145351/13.  
 XX  
 PT Regulating gastrointestinal motility using exendins or their agonists -  
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
 PT glucose tolerance etc., also in diagnostic investigations.  
 XX  
 PS Example 4; Fig 8; 70pp; English.  
 XX  
 CC The present sequence is an exendin agonist, which reduces gastric  
 CC motility and delays gastric emptying. It can be used to treat spasm  
 CC (where associated with acute diverticulitis or disorders of the biliary  
 CC tract or sphincter of Oddi), postprandial dumping syndrome and  
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
 CC is administered to prevent stomach contents passing into the intestines,  
 CC then the stomach pumped) and obesity. It can also be administered to  
 CC subjects undergoing gastrointestinal diagnostic investigation,  
 CC particularly radiological or by magnetic resonance imaging. Exendins,  
 CC components of Gila monster venom, have some sequence similarity to  
 CC glucagon-like peptides (GLP). They are GLP agonists and have been  
 CC suggested (US5424286) for treatment of diabetes and prevention of  
 CC hyperglycaemia  
 XX  
 SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10  
 :| ::||||  
 Db 8 LLFIEFPPPP 17

RESULT 14  
 AAY03738  
 ID AAY03738 standard; peptide; 18 AA.  
 XX  
 AC AAY03738;

XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Exendin agonist compound 18.  
 XX  
 KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
 KW diagnostic; gastro-intestinal; radiological.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "C-terminal amide"  
 XX  
 PN WO9907404-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US016387.  
 XX  
 PR 08-AUG-1997; 97US-0055404P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1999-180403/15.  
 XX  
 PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
 XX  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 XX  
 CC The invention relates to exendin agonists which slow gastric emptying and  
 CC lower plasma glucose levels. The exendin agonists are used to treat Type  
 CC I and II diabetes, disorders which would be benefited by agents which  
 CC lower plasma glucose levels, and disorders which would be benefited by  
 CC agents useful in delaying and/or slowing gastric emptying. Delayed  
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
 CC radiological examinations. Sequences AAY03721-51 represent specifically  
 CC claimed examples of the exendin agonist compounds of the invention. (Also  
 CC see AAY03720 for exendin generic peptide formula and description)  
 XX  
 SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10  
 :| ::|||||  
 Db 8 LLFVEFPPPP 17

RESULT 15  
 AAY03721  
 ID AAY03721 standard; peptide; 18 AA.  
 XX

AC AAY03721;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Exendin agonist compound 1.  
 XX  
 KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
 KW diagnostic; gastro-intestinal; radiological.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "C-terminal amide"  
 XX  
 PN WO9907404-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US016387.  
 XX  
 PR 08-AUG-1997; 97US-0055404P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1999-180403/15.  
 XX  
 PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
 XX  
 PS Claim 17; Fig 1A-B; 70pp; English.  
 XX  
 CC The invention relates to exendin agonists which slow gastric emptying and  
 CC lower plasma glucose levels. The exendin agonists are used to treat Type  
 CC I and II diabetes, disorders which would be benefited by agents which  
 CC lower plasma glucose levels, and disorders which would be benefited by  
 CC agents useful in delaying and/or slowing gastric emptying. Delayed  
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
 CC radiological examinations. Sequences AAY03721-51 represent specifically  
 CC claimed examples of the exendin agonist compounds of the invention. (Also  
 CC see AAY03720 for exendin generic peptide formula and description)  
 XX  
 SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10  
 :| ::|||||  
 Db 8 LLFIEFPPPP 17

RESULT 16  
 AAB52880  
 ID AAB52880 standard; peptide; 18 AA.

XX  
 AC AAB52880;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Extendin agonist compound #8.  
 XX  
 KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
 KW insulin-resistance syndrome; food intake.  
 XX  
 OS Heloderma sp.  
 XX  
 PN WO200066629-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-US011814.  
 XX  
 PR 30-APR-1999; 99US-0132018P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young A, Prickett K;  
 XX  
 DR WPI; 2000-672834/65.  
 XX  
 PT Modified exendin or an exendin agonist linked to one or more polyethylene  
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
 PT treating disorders such as diabetes and obesity.  
 XX  
 PS Disclosure; Fig 3; 119pp; English.  
 XX  
 CC The present invention relates to extendins and their agonists which have  
 CC been modified with molecular weight increasing agents such as  
 CC polyethylene glycol (PEG). These can be used in the treatment of  
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
 XX  
 SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10  
 :| ::||||  
 Db 8 LLFIEFPPPP 17

RESULT 17  
 AAB52886  
 ID AAB52886 standard; peptide; 18 AA.  
 XX  
 AC AAB52886;  
 XX  
 DT 28-FEB-2001 (first entry)



XX  
 DE Extendin agonist compound #14.  
 XX  
 KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
 KW insulin-resistance syndrome; food intake.  
 XX  
 OS Heloderma sp.  
 XX  
 PN WO200066629-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-US011814.  
 XX  
 PR 30-APR-1999; 99US-0132018P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young A, Prickett K;  
 XX  
 DR WPI; 2000-672834/65.  
 XX  
 PT Modified exendin or an exendin agonist linked to one or more polyethylene  
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
 PT treating disorders such as diabetes and obesity.  
 XX  
 PS Disclosure; Fig 3; 119pp; English.  
 XX  
 CC The present invention relates to extendins and their agonists which have  
 CC been modified with molecular weight increasing agents such as  
 CC polyethylene glycol (PEG). These can be used in the treatment of  
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
 XX  
 SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10  
 :| ::|||||  
 Db 8 LLFIEFPPPP 17

# RESULT 18

AAB52876

ID AAB52876 standard; peptide; 18 AA.

XX

AC AAB52876;

XX

DT 28-FEB-2001 (first entry)

XX

DE Extendin agonist compound #4.

XX

KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;

KW insulin-resistance syndrome; food intake.

XX

OS Heloderma sp.

XX

PN WO200066629-A1.

XX

PD 09-NOV-2000.

XX

PF 28-APR-2000; 2000WO-US011814.

XX

PR 30-APR-1999; 99US-0132018P.

XX

PA (AMYL-) AMYLIN PHARM INC.

XX

PI Young A, Prickett K;

XX

DR WPI; 2000-672834/65.

XX

PT Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity.

XX

PS Disclosure; Fig 3; 119pp; English.

XX

CC The present invention relates to extendins and their agonists which have been modified with molecular weight increasing agents such as polyethylene glycol (PEG). These can be used in the treatment of diabetes, obesity, impaired glucose tolerance, postprandial dumping syndrome, postprandial hyperglycaemia, eating disorders, insulin resistance syndrome, dyslipidaemia and to suppress glucagon secretion

XX

SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;

Best Local Similarity 60.0%; Pred. No. 99;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10

:| ::||||

Db 8 LLFVEFPPPP 17

RESULT 19

AAB52885

ID AAB52885 standard; peptide; 18 AA.

XX

AC AAB52885;

XX

DT 28-FEB-2001 (first entry)

XX

DE Extendin agonist compound #13.

XX

KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
KW insulin-resistance syndrome; food intake.

XX

OS Heloderma sp.

XX

PN WO200066629-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-US011814.  
 XX  
 PR 30-APR-1999; 99US-0132018P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young A, Prickett K;  
 XX  
 DR WPI; 2000-672834/65.  
 XX  
 PT Modified exendin or an exendin agonist linked to one or more polyethylene  
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
 PT treating disorders such as diabetes and obesity.  
 XX  
 PS Disclosure; Fig 3; 119pp; English.  
 XX  
 CC The present invention relates to extendins and their agonists which have  
 CC been modified with molecular weight increasing agents such as  
 CC polyethylene glycol (PEG). These can be used in the treatment of  
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
 XX  
 SQ Sequence 18 AA;

Query Match 46.9%; Score 38; DB 3; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 99;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPP 10  
 :| ::|||||  
 Db 8 LLFIEFPPPP 17

# RESULT 20

ABG72860

ID ABG72860 standard; peptide; 15 AA.

XX

AC ABG72860;

XX

DT 26-FEB-2003 (first entry)

XX

DE Human ribosomal protein 17.05 N-terminal.

XX

KW Human; ribosomal protein 17.05; malignant tumour; haemopathy;

KW human immunodeficiency virus; HIV; immunological disease; inflammation.

XX

OS Homo sapiens.

XX

PN CN1352106-A.

XX

PD 05-JUN-2002.

XX

PF 06-NOV-2000; 2000CN-00127235.  
 XX  
 PR 06-NOV-2000; 2000CN-00127235.  
 XX  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-683308/74.  
 XX  
 PT New human ribosomal protein 17.05 polypeptide for treating malignant  
 PT tumors, hemopathy, human immunodeficiency virus infection, immunological  
 PT diseases and various inflammations.  
 XX  
 PS Example 5; Page 18 (Disclosure); 33pp; Chinese.  
 XX  
 CC The present invention discloses a new kind of polypeptide, human  
 CC ribosomal protein 17.05, polynucleotides encoding the polypeptide and a  
 CC DNA recombination process to produce the polypeptide. The present  
 CC invention also describes applying the polypeptide in treating various  
 CC diseases, such as malignant tumours, haemopathy, human immunodeficiency  
 CC virus (HIV) infection, immunological diseases and various inflammations.  
 CC Also discloses is the antagonist resisting the polypeptide and its  
 CC treatment effect, and the application of the polynucleotides encoding  
 CC human ribosomal protein 17.05. This is the amino acid sequence of the  
 CC novel human ribosomal protein 17.05 N-terminal  
 XX  
 SQ Sequence 15 AA;

Query Match 45.7%; Score 37; DB 5; Length 15;  
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 MKFPPPPQETV 14  
 : ||||: |  
 Db 3 VSFPPPPKGQV 13

#### RESULT 21

AAW05469

ID AAW05469 standard; peptide; 18 AA.

XX

AC AAW05469;

XX

DT 24-FEB-1998 (first entry)

XX

DE SH3-binding peptide bSH3020.

XX

KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
 KW cellular signalling element; cellular structural element; malignancy;  
 KW protein identification; functional domain; protein screening;  
 KW cellular signal transduction process; binding peptide.

XX

OS Synthetic.

XX

PN WO9631625-A1.

XX

PD 10-OCT-1996.  
 XX  
 PF 04-APR-1996; 96WO-US004454.  
 XX  
 PR 07-APR-1995; 95US-00417872.  
 PR 03-APR-1996; 96US-00630915.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;  
 XX  
 DR WPI; 1996-465045/46.  
 XX  
 PT Identifying polypeptide(s) having specific functional domain (esp. SH3  
 PT domain) - comprises detecting selective binding to recognition unit,  
 PT regardless of sequence homology.  
 XX  
 PS Example; Fig 12B; 174pp; English.  
 XX  
 CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding  
 CC peptides. These sequences were used as parts of multivalent recognition  
 CC unit complexes used in the method of the invention. The method of the  
 CC invention is for identifying polypeptides containing functional domains  
 CC of interest (especially SH3 domains). It comprises contacting a  
 CC multivalent recognition unit (RU) complex with a number of peptides and  
 CC identifying polypeptides having a selective binding affinity for the RU  
 CC complex. The method is based on functional similarities and does not rely  
 CC on sequence similarities. Prior methods only gave limited success for  
 CC identifying proteins containing an SH3 domain due to the minimal sequence  
 CC homology among known SH3 proteins. Multivalent RU complexes are  
 CC particularly suited to screening for polypeptides containing functional  
 CC domains that are similar to, but not identical in sequence to, the  
 CC original target functional domain. The new method enables proteins having  
 CC a common function to be identified. Identification of novel SH3 proteins  
 CC will be useful for a better understanding of cell growth, malignancy,  
 CC signal transduction processes, etc. New candidate drugs can be  
 CC identified, and their specificities (e.g. pharmacological activities) can  
 CC be assessed using the method of the invention  
 XX  
 SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
 | |||| :  
 Db 7 EPDFPPPPPD 16

RESULT 22  
 AAW37677  
 ID AAW37677 standard; peptide; 18 AA.  
 XX  
 AC AAW37677;  
 XX

DT 23-APR-1998 (first entry)  
 XX  
 DE PPPPY motif containing peptide bSH3020 used to bind WW domains.  
 XX  
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;  
 KW cytoskeleton organisation; targeted drug screening; modulator;  
 KW WW domain interaction; YAP protein; dystrophin.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9737223-A1.  
 XX  
 PD 09-OCT-1997.  
 XX  
 PF 03-APR-1997; 97WO-US005547.  
 XX  
 PR 03-APR-1996; 96US-00630916.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Pirozzi G, Kay BK, Fowlkes DM;  
 XX  
 DR WPI; 1997-503234/46.  
 XX  
 PT Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are useful  
 PT in targetted drug selection.  
 XX  
 PS Example 6.3; Fig 7; 220pp; English.  
 XX  
 CC Peptides AAW37653-77 contain PPPPY-like motifs. The PPPY motif is found  
 CC in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides  
 CC containing this residue have been shown to bind the YAP WW domain, but  
 CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides  
 CC AAW37653-77 were biotinylated and complexed with alkaline streptavidin,  
 CC and used in a cross affinity mapping experiment. They were tested for  
 CC their ability to bind to the 12 individual novel WW domains of WWP1  
 CC (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which  
 CC were expressed as glutathione-S-transferase expression proteins. The  
 CC present peptide, derived from a vinculin protein, does not bind to WW  
 CC domains of the novel proteins. The WW domain is a small functional  
 CC domain. Its name is derived from the observation that two tryptophan  
 CC residues, one in the amino terminal portion of the WW domain and one in  
 CC the carboxyl terminal portion, are conserved. Most proteins containing WW  
 CC domains have a function involving cell signalling and growth regulation  
 CC or the organisation of the cytoskeleton. Polypeptides containing a WW  
 CC domain are identified by treating a multivalent recognition unit complex  
 CC that has selective binding affinity for a WW domain, with many  
 CC polypeptides and identifying those with selective affinity for the  
 CC complex. Proteins containing WW domains are used for targeted drug  
 CC screening, i.e. to identify potential modulators of specific WW domain  
 CC interactions  
 XX  
 SQ Sequence 18 AA;

Query Match

45.7%; Score 37; DB 2; Length 18;

Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
| |||| :  
Db 7 EPDFPPPPPD 16

RESULT 23

AAW38909

ID AAW38909 standard; peptide; 18 AA.

XX

AC AAW38909;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;

KW PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US002298.

XX

PR 16-FEB-1996; 96US-00602999.

XX

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JE;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src tyrosine  
PT kinase(s) and to stimulate immune response by increasing production of  
PT certain lymphokine(s), e.g. interleukin-1.

XX

PS Claim 22; Page 90; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology  
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain  
CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
CC can be used in the method to identify inhibitors of their binding to  
CC their respective SH3 domains, which could be used to modulate the

CC pharmacological activity of proteins or polypeptide containing the SH3  
CC domain. The peptides can also be used to activate Src or Src-related  
CC protein tyrosine kinases, to stimulate the immune response by increasing  
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
CC and interleukin-1, or to deliver a conjugated molecule to certain  
CC cellular compartments containing Src or Src related proteins  
XX  
SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPPQETV 14  
| | | | : :  
Db 7 FPPPPYQPI 15

RESULT 24

AAW47562

ID AAW47562 standard; peptide; 18 AA.

XX

AC AAW47562;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (13).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;

KW postprandial dumping syndrome; postprandial hyperglycaemia;

KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;

KW Gila monster venom.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 8

FT /note= "pentylglycine"

FT Modified-site 18

FT /note= "amidated"

XX

PN WO9805351-A1.

XX

PD 12-FEB-1998.

XX

PF 08-AUG-1997; 97WO-US014199.

XX

PR 08-AUG-1996; 96US-00694954.

XX

PA (AMYL-) AMYLIN PHARM INC.

XX

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX

DR WPI; 1998-145351/13.

XX

PT Regulating gastrointestinal motility using exendins or their agonists -

PT for treating spasm, diabetic postprandial hyperglycaemia, impaired



PT glucose tolerance etc., also in diagnostic investigations.

XX

PS Example 16; Fig 8; 70pp; English.

XX

CC The present sequence is an exendin agonist, which reduces gastric  
CC motility and delays gastric emptying. It can be used to treat spasm  
CC (where associated with acute diverticulitis or disorders of the biliary  
CC tract or sphincter of Oddi), postprandial dumping syndrome and  
CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
CC is administered to prevent stomach contents passing into the intestines,  
CC then the stomach pumped) and obesity. It can also be administered to  
CC subjects undergoing gastrointestinal diagnostic investigation,  
CC particularly radiological or by magnetic resonance imaging. Exendins,  
CC components of Gila monster venom, have some sequence similarity to  
CC glucagon-like peptides (GLP). They are GLP agonists and have been  
CC suggested (US5424286) for treatment of diabetes and prevention of  
CC hyperglycaemia

XX

SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LEMKFPPPP 10

| ::|||||

Db 9 LFIEFPPPP 17

#### RESULT 25

AAY03733

ID AAY03733 standard; peptide; 18 AA.

XX

AC AAY03733;

XX

DT 08-JUN-1999 (first entry)

XX

DE Exendin agonist compound 13.

XX

KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
KW diagnostic; gastro-intestinal; radiological.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 8

FT /note= "pentylglycine"

FT Modified-site 18

FT /note= "C-terminal amide"

XX

PN WO9907404-A1.

XX

PD 18-FEB-1999.

XX

PF 06-AUG-1998; 98WO-US016387.

XX

PR 08-AUG-1997; 97US-0055404P.  
XX  
PA (AMYL-) AMYLIN PHARM INC.  
XX  
PI Beeley NRA, Prickett KS;  
XX  
DR WPI; 1999-180403/15.  
XX  
PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
XX  
PS Claim 17; Fig 1A-B; 70pp; English.  
XX  
CC The invention relates to exendin agonists which slow gastric emptying and  
CC lower plasma glucose levels. The exendin agonists are used to treat Type  
CC I and II diabetes, disorders which would be benefited by agents which  
CC lower plasma glucose levels, and disorders which would be benefited by  
CC agents useful in delaying and/or slowing gastric emptying. Delayed  
CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
CC radiological examinations. Sequences AAY03721-51 represent specifically  
CC claimed examples of the exendin agonist compounds of the invention. (Also  
CC see AAY03720 for exendin generic peptide formula and description)  
XX  
SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKFPPPP 10  
| ::|||||  
Db 9 LFIEFPPPP 17

#### RESULT 26

ADB49303

ID ADB49303 standard; peptide; 18 AA.

XX

AC ADB49303;

XX

DT 04-DEC-2003 (first entry)

XX

DE Novel WW domain binding peptide #25.

XX

KW WW domain; drug candidate screening; drug discovery; drug modification;

KW drug refinement; immunogen; WW binding protein; WW domain.

XX

OS Unidentified.

XX

PN US2003077577-A1.

XX

PD 24-APR-2003.

XX

PF 28-JUN-2002; 2002US-00185050.

XX

PR 03-APR-1996; 96US-00630916.

PR 03-APR-1997; 97US-00826516.

XX

PA (PIRO/) PIROZZI G.  
PA (KAYB/) KAY B K.  
PA (FOWL/) FOWLKES D M.

XX

PI Pirozzi G, Kay BK, Fowlkes DM;

XX

DR WPI; 2003-635075/60.

XX

PT Novel purified polypeptide comprising WW domain, useful for drug  
PT discovery, modification and refinement, for discovering polypeptides  
PT involved in pharmacological activities, or as an immunogen to generate  
PT antibodies.

XX

PS Example; Fig 7; 133pp; English.

XX

CC The invention describes a purified polypeptide (I) comprising a WW domain  
CC which has a sequence (S1) selected from 11 sequences fully defined in the  
CC specification, a sequence (S2) selected from 48 sequences fully defined  
CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725  
CC amino acids fully defined in the specification. (I) is useful for  
CC screening a potential drug candidate, by allowing (I) to come into  
CC contact with at least one recognition unit having a selective affinity  
CC for the WW domain in (I), in the presence of an amount of a potential  
CC drug candidate, such that (I) and the recognition unit are capable of  
CC interacting when brought into contact with one another in the absence of  
CC the drug candidate, and determining the effect, if any, of the presence  
CC of the amount of the drug candidate on the interaction of (I) with the  
CC recognition unit. (I) is useful for drug discovery, modification and  
CC refinement, for discovering polypeptides involved in pharmacological  
CC activities, or as an immunogen to generate antibodies. This is the amino  
CC acid sequence of a peptide that binds the novel WW domains of the  
CC invention

XX

SQ Sequence 18 AA;

Query Match 45.7%; Score 37; DB 7; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
| ||||| :  
Db 7 EPDFPPPPPD 16

#### RESULT 27

AAR07284

ID AAR07284 standard; protein; 10 AA.

XX

AC AAR07284;

XX

DT 31-JAN-1991 (first entry)

XX

DE Smooth muscle myosin-2 immunogen for antibody prodn.

XX

KW Smooth muscle myosin isoform 2; monoclonal antibody; immunogen;  
KW diagnosis; arteriosclerosis.

XX

OS Homo sapiens.  
 XX  
 PN WO9011520-A.  
 XX  
 PD 04-OCT-1990.  
 XX  
 PF 28-MAR-1989; 89JP-00075884.  
 XX  
 PR 28-MAR-1989; 89JP-00075884.  
 XX  
 PA (YAMS ) YAMASA SHOYU KK.  
 XX  
 PI Nagai R, Kuroo M, Kato H;  
 XX  
 DR WPI; 1990-320366/42.  
 XX  
 PT Antibody against heavy chain of smooth muscle myosin - as reagent for  
 PT histological staining of smooth muscle or diagnosis of blood vessel  
 PT disorders.  
 XX  
 PS Claim 7; Page 42; 61pp; Japanese.  
 XX  
 CC The oligopeptide is used as immunogen for the prodn. of monoclonal  
 CC antibodies recognising isoform SM-2 of the heavy chain of smooth muscle  
 CC myosin, pref. from heart or skeletal muscle, esp. human. The peptide  
 CC contains the part which differs between isoforms SM1-3. The antibodies  
 CC may be obtained by immunisation with the immunogen, followed by cell  
 CC fusion to produce a hybridoma, cloning and culturing the chosen hybridoma  
 CC clone. The Ab is a reagent for the histological staining of smooth  
 CC muscle, and is useful in the diagnosis of arteriosclerosis, blood vessel  
 CC disorders etc. See also AAR07283-5  
 XX  
 SQ Sequence 10 AA;

Query Match 44.4%; Score 36; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPQET 13  
 |||||  
 Db 3 PPPQET 8

# RESULT 28

AAG79174

ID AAG79174 standard; peptide; 14 AA.

XX

AC AAG79174;

XX

DT 03-JAN-2002 (first entry)

XX

DE Peptide derived from ActA, and containing EVH1-binding site.

XX

KW ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;

KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;

KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;

KW infectious disease; cancer; autoimmune disease; inflammation;

KW platelet aggregation; wound healing; clotting.

XX

OS *Listeria monocytogenes*.

XX

PN WO200174858-A2.

XX

PD 11-OCT-2001.

XX

PF 03-APR-2001; 2001WO-US010753.

XX

PR 03-APR-2000; 2000US-0194215P.

XX

PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.

PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX

PI Krause M, Sechi AS, Gertler FB, Wehland J;

XX

DR WPI; 2001-616686/71.

XX

PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage

PT activation for treating cancer, autoimmune disease, and infectious

PT disease, comprises contacting with a Fyb/SLAP complex modulator.

XX

PS Example 5; Page 43; 79pp; English.

XX

CC The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are  
CC ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated  
CC phosphoprotein (VASP) proteins. The specification describes a method for  
CC modulating cytoskeletal rearrangement in a cell, or T cell response to T  
CC cell receptor stimulation. The method comprises contacting the cell or T  
CC cell with a Fyb/SLAP complex modulator sufficient to modulate the  
CC formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The  
CC method is useful for modulating cytoskeletal rearrangement in a cell such  
CC as a lymphocyte, preferably a T cell, a macrophage or a cell fragment  
CC such as a platelet and for modulating T cell response to a T cell  
CC receptor stimulation. T cell response is increased in a subject having or  
CC at risk of developing infectious disease or cancer and T cell response is  
CC inhibited in a subject having or is at risk of developing an autoimmune  
CC disease or a condition characterized by inflammation. A composition  
CC comprising a Fyb/SLAP complex inhibitor is useful for increasing platelet  
CC aggregation for promoting wound healing or clotting. The present sequence  
CC represents a peptide derived from ActA, which is used in the course of  
CC the invention

XX

SQ Sequence 14 AA;

Query Match 44.4%; Score 36; DB 4; Length 14;

Best Local Similarity 62.5%; Pred. No. 1.5e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPPQE 12

:||||:

Db 2 EFPPPTD 9

RESULT 29

AAG79166

ID AAG79166 standard; peptide; 15 AA.  
XX  
AC AAG79166;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Synthetic antigenic peptide derived from ActA.  
XX  
KW ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
KW infectious disease; cancer; autoimmune disease; inflammation;  
KW platelet aggregation; wound healing; clotting.  
XX  
OS Synthetic.  
OS Listeria monocytogenes.  
XX  
PN WO200174858-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010753.  
XX  
PR 03-APR-2000; 2000US-0194215P.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Krause M, Sechi AS, Gertler FB, Wehland J;  
XX  
DR WPI; 2001-616686/71.  
XX  
PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage  
PT activation for treating cancer, autoimmune disease, and infectious  
PT disease, comprises contacting with a Fyb/SLAP complex modulator.  
XX  
PS Example 1; Page 36; 79pp; English.  
XX  
CC The present sequence represents an antigenic peptide derived from ActA.  
CC polyclonal antibodies raised against this peptide were used to screen  
CC mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP  
CC proteins are ligands for the EVH1 domains of Ena(enabled)/vasodilator-  
CC stimulated phosphoprotein (VASP) proteins. The specification describes a  
CC method for modulating cytoskeletal rearrangement in a cell, or T cell  
CC response to T cell receptor stimulation. The method comprises contacting  
CC the cell or T cell with a Fyb/SLAP complex modulator sufficient to  
CC modulate the formation of a complex of an Ena/VASP protein and a Fyb/SLAP  
CC protein. The method is useful for modulating cytoskeletal rearrangement  
CC in a cell such as a lymphocyte, preferably a T cell, a macrophage or a  
CC cell fragment such as a platelet and for modulating T cell response to a  
CC T cell receptor stimulation. T cell response is increased in a subject  
CC having or at risk of developing infectious disease or cancer and T cell  
CC response is inhibited in a subject having or is at risk of developing an  
CC autoimmune disease or a condition characterized by inflammation. A  
CC composition comprising a Fyb/SLAP complex inhibitor is useful for  
CC increasing platelet aggregation for promoting wound healing or clotting  
XX

SQ Sequence 15 AA;

Query Match 44.4%; Score 36; DB 4; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPPQE 12  
:||||| :  
Db 3 EFPPPPPTD 10

RESULT 30

AAW47569

ID AAW47569 standard; peptide; 18 AA.

XX

AC AAW47569;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (20).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;

KW postprandial dumping syndrome; postprandial hyperglycaemia;

KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;

KW Gila monster venom.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "tert-butylglycine"

FT Modified-site 18

FT /note= "amidated"

XX

PN WO9805351-A1.

XX

PD 12-FEB-1998.

XX

PF 08-AUG-1997; 97WO-US014199.

XX

PR 08-AUG-1996; 96US-00694954.

XX

PA (AMYL-) AMYLIN PHARM INC.

XX

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX

DR WPI; 1998-145351/13.

XX

PT Regulating gastrointestinal motility using exendins or their agonists -

PT for treating spasm, diabetic postprandial hyperglycaemia, impaired

PT glucose tolerance etc., also in diagnostic investigations.

XX

PS Example 23; Fig 8; 70pp; English.

XX

CC The present sequence is an exendin agonist, which reduces gastric

CC motility and delays gastric emptying. It can be used to treat spasm

CC (where associated with acute diverticulitis or disorders of the biliary

CC tract or sphincter of Oddi), postprandial dumping syndrome and  
CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
CC is administered to prevent stomach contents passing into the intestines,  
CC then the stomach pumped) and obesity. It can also be administered to  
CC subjects undergoing gastrointestinal diagnostic investigation,  
CC particularly radiological or by magnetic resonance imaging. Exendins,  
CC components of Gila monster venom, have some sequence similarity to  
CC glucagon-like peptides (GLP). They are GLP agonists and have been  
CC suggested (US5424286) for treatment of diabetes and prevention of  
CC hyperglycaemia

XX

SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10  
:| :||||  
Db 8 LLFXEFPPPP 17

RESULT 31

AAW47552

ID AAW47552 standard; peptide; 18 AA.

XX

AC AAW47552;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (3).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;  
KW postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;  
KW Gila monster venom.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "amidated"

XX

PN WO9805351-A1.

XX

PD 12-FEB-1998.

XX

PF 08-AUG-1997; 97WO-US014199.

XX

PR 08-AUG-1996; 96US-00694954.

XX

PA (AMYL-) AMYLIN PHARM INC.

XX

PI Young AA, Gedulin B, Beeley NRA, Prickett KS;

XX

DR WPI; 1998-145351/13.



XX  
PT Regulating gastrointestinal motility using exendins or their agonists -  
PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
PT glucose tolerance etc., also in diagnostic investigations.  
XX  
PS Example 6; Fig 8; 70pp; English.  
XX  
CC The present sequence is an exendin agonist, which reduces gastric  
CC motility and delays gastric emptying. It can be used to treat spasm  
CC (where associated with acute diverticulitis or disorders of the biliary  
CC tract or sphincter of Oddi), postprandial dumping syndrome and  
CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
CC is administered to prevent stomach contents passing into the intestines,  
CC then the stomach pumped) and obesity. It can also be administered to  
CC subjects undergoing gastrointestinal diagnostic investigation,  
CC particularly radiological or by magnetic resonance imaging. Exendins,  
CC components of Gila monster venom, have some sequence similarity to  
CC glucagon-like peptides (GLP). They are GLP agonists and have been  
CC suggested (US5424286) for treatment of diabetes and prevention of  
CC hyperglycaemia  
XX  
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFPPPP 10  
::|||||  
Db 11 IEFPPPP 17

# RESULT 32

AAW47564

ID AAW47564 standard; peptide; 18 AA.

XX

AC AAW47564;

XX

DT 03-JUL-1998 (first entry)

XX

DE Exendin agonist (15).

XX

KW Exendin agonist; gastric motility; gastric emptying; treatment; spasm;  
KW postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity;  
KW Gila monster venom.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 9

FT /note= "pentylglycine"

FT Modified-site 18

FT /note= "amidated"

XX

PN WO9805351-A1.

XX  
 PD 12-FEB-1998.  
 XX  
 PF 08-AUG-1997; 97WO-US014199.  
 XX  
 PR 08-AUG-1996; 96US-00694954.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young AA, Gedulin B, Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1998-145351/13.  
 XX  
 PT Regulating gastrointestinal motility using exendins or their agonists -  
 PT for treating spasm, diabetic postprandial hyperglycaemia, impaired  
 PT glucose tolerance etc., also in diagnostic investigations.  
 XX  
 PS Example 18; Fig 8; 70pp; English.  
 XX  
 CC The present sequence is an exendin agonist, which reduces gastric  
 CC motility and delays gastric emptying. It can be used to treat spasm  
 CC (where associated with acute diverticulitis or disorders of the biliary  
 CC tract or sphincter of Oddi), postprandial dumping syndrome and  
 CC hyperglycaemia (particularly associated with type 2 diabetes), type 1  
 CC diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist  
 CC is administered to prevent stomach contents passing into the intestines,  
 CC then the stomach pumped) and obesity. It can also be administered to  
 CC subjects undergoing gastrointestinal diagnostic investigation,  
 CC particularly radiological or by magnetic resonance imaging. Exendins,  
 CC components of Gila monster venom, have some sequence similarity to  
 CC glucagon-like peptides (GLP). They are GLP agonists and have been  
 CC suggested (US5424286) for treatment of diabetes and prevention of  
 CC hyperglycaemia  
 XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
 : : | | | |  
 Db 11 IEFPPPP 17

# RESULT 33

AAY03740

ID AAY03740 standard; peptide; 18 AA.

XX

AC AAY03740;

XX

DT 08-JUN-1999 (first entry)

XX

DE Exendin agonist compound 20.

XX

KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
 KW diagnostic; gastro-intestinal; radiological.

XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 11  
 FT /note= "tert-butylglycine"  
 FT Modified-site 18  
 FT /note= "C-terminal amide"  
 XX  
 PN WO9907404-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US016387.  
 XX  
 PR 08-AUG-1997; 97US-0055404P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1999-180403/15.  
 XX  
 PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
 XX  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 XX  
 CC The invention relates to exendin agonists which slow gastric emptying and  
 CC lower plasma glucose levels. The exendin agonists are used to treat Type  
 CC I and II diabetes, disorders which would be benefited by agents which  
 CC lower plasma glucose levels, and disorders which would be benefited by  
 CC agents useful in delaying and/or slowing gastric emptying. Delayed  
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
 CC radiological examinations. Sequences AAY03721-51 represent specifically  
 CC claimed examples of the exendin agonist compounds of the invention. (Also  
 CC see AAY03720 for exendin generic peptide formula and description)  
 XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10  
 :| :||||  
 Db 8 LLFXEFPPPP 17

RESULT 34  
 AAY03723  
 ID AAY03723 standard; peptide; 18 AA.  
 XX  
 AC AAY03723;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX  
 DE Exendin agonist compound 3.

XX  
 KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
 KW diagnostic; gastro-intestinal; radiological.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "C-terminal amide"  
 XX  
 PN WO9907404-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US016387.  
 XX  
 PR 08-AUG-1997; 97US-0055404P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1999-180403/15.  
 XX  
 PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
 XX  
 PS Claim 17; Fig 1A-B; 70pp; English.  
 XX  
 CC The invention relates to exendin agonists which slow gastric emptying and  
 CC lower plasma glucose levels. The exendin agonists are used to treat Type  
 CC I and II diabetes, disorders which would be benefited by agents which  
 CC lower plasma glucose levels, and disorders which would be benefited by  
 CC agents useful in delaying and/or slowing gastric emptying. Delayed  
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
 CC radiological examinations. Sequences AAY03721-51 represent specifically  
 CC claimed examples of the exendin agonist compounds of the invention. (Also  
 CC see AAY03720 for exendin generic peptide formula and description)  
 XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
 : : | | | |  
 Db 11 IEFPPPP 17

RESULT 35  
 AAY03742  
 ID AAY03742 standard; peptide; 18 AA.  
 XX  
 AC AAY03742;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX

DE Exendin agonist compound 22.  
 XX  
 KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
 KW diagnostic; gastro-intestinal; radiological.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "C-terminal amide"  
 XX  
 PN WO9907404-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US016387.  
 XX  
 PR 08-AUG-1997; 97US-0055404P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Beeley NRA, Prickett KS;  
 XX  
 DR WPI; 1999-180403/15.  
 XX  
 PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
 XX  
 PS Claim 17; Fig 1D-E; 70pp; English.  
 XX  
 CC The invention relates to exendin agonists which slow gastric emptying and  
 CC lower plasma glucose levels. The exendin agonists are used to treat Type  
 CC I and II diabetes, disorders which would be benefited by agents which  
 CC lower plasma glucose levels, and disorders which would be benefited by  
 CC agents useful in delaying and/or slowing gastric emptying. Delayed  
 CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
 CC radiological examinations. Sequences AAY03721-51 represent specifically  
 CC claimed examples of the exendin agonist compounds of the invention. (Also  
 CC see AAY03720 for exendin generic peptide formula and description)  
 XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
 ::|||||  
 Db 11 IEFPPPP 17

RESULT 36  
 AAY03735  
 ID AAY03735 standard; peptide; 18 AA.  
 XX  
 AC AAY03735;  
 XX  
 DT 08-JUN-1999 (first entry)

XX  
DE Exendin agonist compound 15.  
XX  
KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;  
KW diagnostic; gastro-intestinal; radiological.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 9  
FT /note= "pentylglycine"  
FT Modified-site 18  
FT /note= "C-terminal amide"  
XX  
PN WO9907404-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 06-AUG-1998; 98WO-US016387.  
XX  
PR 08-AUG-1997; 97US-0055404P.  
XX  
PA (AMYL-) AMYLIN PHARM INC.  
XX  
PI Beeley NRA, Prickett KS;  
XX  
DR WPI; 1999-180403/15.  
XX  
PT New exendin agonists - useful in the treatment of Type I and II diabetes.  
XX  
PS Claim 17; Fig 1D-E; 70pp; English.  
XX  
CC The invention relates to exendin agonists which slow gastric emptying and  
CC lower plasma glucose levels. The exendin agonists are used to treat Type  
CC I and II diabetes, disorders which would be benefited by agents which  
CC lower plasma glucose levels, and disorders which would be benefited by  
CC agents useful in delaying and/or slowing gastric emptying. Delayed  
CC gastric emptying is a useful diagnostic aid in gastro-intestinal  
CC radiological examinations. Sequences AAY03721-51 represent specifically  
CC claimed examples of the exendin agonist compounds of the invention. (Also  
CC see AAY03720 for exendin generic peptide formula and description)  
XX  
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
::|||||  
Db 11 IEFPPPP 17

RESULT 37  
AAB52878  
ID AAB52878 standard; peptide; 18 AA.  
XX

AC AAB52878;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Extendin agonist compound #6.  
 XX  
 KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
 KW insulin-resistance syndrome; food intake.  
 XX  
 OS Heloderma sp.  
 XX  
 PN WO200066629-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-US011814.  
 XX  
 PR 30-APR-1999; 99US-0132018P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young A, Prickett K;  
 XX  
 DR WPI; 2000-672834/65.  
 XX  
 PT Modified exendin or an exendin agonist linked to one or more polyethylene  
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
 PT treating disorders such as diabetes and obesity.  
 XX  
 PS Disclosure; Fig 3; 119pp; English.  
 XX  
 CC The present invention relates to extendins and their agonists which have  
 CC been modified with molecular weight increasing agents such as  
 CC polyethylene glycol (PEG). These can be used in the treatment of  
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
 XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 3; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLEMKFPPPP 10  
 :| :||||  
 Db 8 LLFXEFPPPP 17

# RESULT 38

AAB52873

ID AAB52873 standard; peptide; 18 AA.

XX

AC AAB52873;

XX

DT 28-FEB-2001 (first entry)

XX

DE Extendin agonist compound #1.  
 XX  
 KW Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia;  
 KW insulin-resistance syndrome; food intake.  
 XX  
 OS Heloderma sp.  
 XX  
 PN WO200066629-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-US011814.  
 XX  
 PR 30-APR-1999; 99US-0132018P.  
 XX  
 PA (AMYL-) AMYLIN PHARM INC.  
 XX  
 PI Young A, Prickett K;  
 XX  
 DR WPI; 2000-672834/65.  
 XX  
 PT Modified exendin or an exendin agonist linked to one or more polyethylene  
 PT glycol (PEG) polymers, modulate plasma glucose levels, useful for  
 PT treating disorders such as diabetes and obesity.  
 XX  
 PS Disclosure; Fig 3; 119pp; English.  
 XX  
 CC The present invention relates to extendins and their agonists which have  
 CC been modified with molecular weight increasing agents such as  
 CC polyethylene glycol (PEG). These can be used in the treatment of  
 CC diabetes, obesity, impaired glucose tolerance, postprandial dumping  
 CC syndrome, postprandial hyperglycaemia, eating disorders, insulin  
 CC resistance syndrome, dyslipidaemia and to suppress glucagon secretion  
 XX  
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 3; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
 ::|||||  
 Db 11 IEFPPPP 17

# RESULT 39

AAW47943

ID AAW47943 standard; peptide; 10 AA.

XX

AC AAW47943;

XX

DT 12-JUN-1998 (first entry)

XX

DE AE101 analogue effector compound SEQ ID NO:19.

XX

KW Mammalian Ii key peptide; mammalian invariant chain protein; allergy;

KW immune response; MHC class II; antigenic; autoimmune disease.



```

XX
OS   Synthetic.
XX
FH   Key           Location/Qualifiers
FT   Modified-site 1
FT                               /note= "Acylated"
FT   Modified-site 10
FT                               /note= "Amidated"
XX
PN   WO9749430-A1.
XX
PD   31-DEC-1997.
XX
PF   09-JUN-1997;   97WO-US009993.
XX
PR   26-JUN-1996;   96US-00670605.
XX
PA   (ANTI-) ANTIGEN EXPRESS INC.
XX
PI   Humphreys RE,  Adams S,  Xu M;
XX
DR   WPI; 1998-076917/07.
XX
PT   New mammalian invariant chain protein (Ii) key peptide(s) - used for
PT   modulation of immune response, e.g. for treating malignant, allergic or
PT   autoimmune disease or allograft rejection.
XX
PS   Example 1; Page 26; 149pp; English.
XX
CC   The present sequence represents an AE101 analogue effector compound used
CC   in the present invention. The present invention describes a mammalian
CC   invariant chain protein (Ii) key peptide of sequence LRMKLPKPPKPVSKMR and
CC   modifications with the exclusion of peptide YRMKLPKPPKPVSKMR. MHC class
CC   II molecules are synthesised in the endoplasmic reticulum with their
CC   antigenic peptide sites blocked by the invariant chain protein (Ii). The
CC   products and method can be used for the modulation of an immune response
CC   for therapeutic or diagnostic purposes. The enhancement of immunity can
CC   be used in the treatment of e.g. malignant or allergic disease. The
CC   immunosuppression can be used for the treatment of autoimmune disease,
CC   e.g. rheumatoid arthritis, multiple sclerosis, diabetes mellitus, lupus
CC   erythematosus, and psoriasis or allograft rejection
XX
SQ   Sequence 10 AA;

      Query Match           43.2%;  Score 35;  DB 2;  Length 10;
      Best Local Similarity  60.0%;  Pred. No. 1.5e+02;
      Matches      6;  Conservative  1;  Mismatches      3;  Indels      0;  Gaps      0;

Qy           2 LEMKFPPPPQ 11
              | || | ||:
Db           1 LRMKLPKPPK 10

RESULT 40
AAU09138
ID   AAU09138 standard; peptide; 10 AA.
XX

```

AC AAU09138;  
 XX  
 DT 19-DEC-2001 (first entry)  
 XX  
 DE Ena/VASP homology (EVH) consensus binding site.  
 XX  
 KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
 KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
 KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
 KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
 KW Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
 KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
 KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
 KW cancer; ischaemia.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /label= Asp, Gly  
 FT Misc-difference 7  
 FT /label= OTHER  
 FT /note= "Other = any amino acid"  
 XX  
 PN WO200174853-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US010249.  
 XX  
 PR 03-APR-2000; 2000US-0194564P.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 XX  
 PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;  
 XX  
 DR WPI; 2001-626380/72.  
 XX  
 PT Regulating cell motility for promoting wound healing and tissue  
 PT regeneration, treating, neurodegenerative disease and metastasis, by  
 PT inducing or depleting a functional enabled/vasodilator-stimulated  
 PT phosphoprotein.  
 XX  
 PS Example 2; Page 59; 107pp; English.  
 XX  
 CC The invention relates to a method of preventing mammalian cell migration,  
 CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
 CC phosphoprotein (VASP) or promoting cell migration comprising depleting  
 CC functional Ena/VASP protein in the mammalian cell. The method is useful  
 CC for preventing or promoting mammalian cell migration, preferably tumour  
 CC cell migration in vitro or in vivo and to prevent tumour cell metastasis  
 CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
 CC wound healing, preferably fibroblasts or nerve cells of a tissue type  
 CC with the inhibitor to promote actin polymerisation and tissue formation  
 CC on a scaffold. The inhibitor is also useful for preventing

CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
CC complex, progressive supranuclear palsy, progressive bulbar palsy,  
CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
CC cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
CC inhibitor is further useful for enhancing learning and memory in a  
CC subject having or at risk of developing a learning disorder such as  
CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
CC is administered in an amount for inhibiting the activity of Mena in a  
CC synapse. Ena/VASP activator is useful for disrupting learning and memory  
CC and the activator is administered in an amount to promote Ena/VASP  
CC protein-FE65 interaction. Inducing the activity of Ena/VASP protein in  
CC immune or haematopoietic cells reduces the ability of the cells to  
CC migrate and this is useful for treating and preventing inflammatory  
CC disorders such as arthritis, allergy, gout, organ transplant, ulcerative  
CC colitis and ischaemic diseases and also for treating cancer metastasis.  
CC The present sequence represents the amino acid sequence of Ena/VASP  
CC homology (EVH) consensus binding site

XX

SQ Sequence 10 AA;

Query Match 43.2%; Score 35; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPPPPQE 12

||||| :

Db 2 FPPPPXD 8

RESULT 41

AAW48084

ID AAW48084 standard; peptide; 12 AA.

XX

AC AAW48084;

XX

DT 12-JUN-1998 (first entry)

XX

DE AE101 series compound peptide SEQ ID NO:161.

XX

KW Mammalian Ii key peptide; mammalian invariant chain protein; allergy;

KW immune response; MHC class II; antigenic; autoimmune disease.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Acylated"

FT Modified-site 12

FT /note= "Amidated"

XX

PN W09749430-A1.

XX

PD 31-DEC-1997.

XX  
 PF 09-JUN-1997; 97WO-US009993.  
 XX  
 PR 26-JUN-1996; 96US-00670605.  
 XX  
 PA (ANTI-) ANTIGEN EXPRESS INC.  
 XX  
 PI Humphreys RE, Adams S, Xu M;  
 XX  
 DR WPI; 1998-076917/07.  
 XX  
 PT New mammalian invariant chain protein (Ii) key peptide(s) - used for  
 PT modulation of immune response, e.g. for treating malignant, allergic or  
 PT autoimmune disease or allograft rejection.  
 XX  
 PS Example 7; Page 83; 149pp; English.  
 XX  
 CC The present sequence represents an AE101 series compound peptide used in  
 CC the present invention. The present invention describes a mammalian  
 CC invariant chain protein (Ii) key peptide of sequence LRMKLPKPPKPVSKMR and  
 CC modifications with the exclusion of peptide YRMKLPKPPKPVSKMR. MHC class  
 CC II molecules are synthesised in the endoplasmic reticulum with their  
 CC antigenic peptide sites blocked by the invariant chain protein (Ii). The  
 CC products and method can be used for the modulation of an immune response  
 CC for therapeutic or diagnostic purposes. The enhancement of immunity can  
 CC be used in the treatment of e.g. malignant or allergic disease. The  
 CC immunosuppression can be used for the treatment of autoimmune disease,  
 CC e.g. rheumatoid arthritis, multiple sclerosis, diabetes mellitus, lupus  
 CC erythematosus, and psoriasis or allograft rejection  
 XX  
 SQ Sequence 12 AA;

Query Match 43.2%; Score 35; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11  
 | ||| ||:  
 Db 1 LRMKLPKPPK 10

#### RESULT 42

AAW38053

ID AAW38053 standard; peptide; 13 AA.

XX

AC AAW38053;

XX

DT 23-APR-1998 (first entry)

XX

DE Peptide recognition unit YP used to identify WW domains.

XX

KW Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;

KW WW domain; cell signalling; growth regulation; cytoskeleton organisation;

KW targeted drug screening; modulator; WW domain interaction.

XX

OS Synthetic.

XX

```

FH      Key                      Location/Qualifiers
FT      Modified-site           1
FT                               /note= "residue is biotinylated"
XX
PN      WO9737223-A1.
XX
PD      09-OCT-1997.
XX
PF      03-APR-1997;           97WO-US005547.
XX
PR      03-APR-1996;           96US-00630916.
XX
PA      (CYTO-) CYTOGEN CORP.
PA      (UYNC-) UNIV NORTH CAROLINA.
XX
PI      Pirozzi G, Kay BK, Fowlkes DM;
XX
DR      WPI; 1997-503234/46.
XX
PT      Identifying cell signalling and growth regulatory polypeptides by
PT      reaction with multivalent recognition complex - polypeptides are useful
PT      in targetted drug selection.
XX
PS      Example 1; Page 67; 220pp; English.
XX
CC      Peptides AAW38052-53 are peptide recognition units that are based on the
CC      sequences of the YAP WW domain binding proteins WBP-1 and WBP-2. They
CC      were used to screen a mouse cDNA expression library. The WW domain is a
CC      small functional domain found in a large number of proteins from a
CC      variety of species including humans, nematodes and yeast. Its name is
CC      derived from the observation that two tryptophan residues, one in the
CC      amino terminal portion of the WW domain and one in the carboxyl terminal
CC      portion, are conserved. Most proteins containing WW domains have a
CC      function involving cell signalling and growth regulation or the
CC      organisation of the cytoskeleton. Polypeptides containing a WW domain are
CC      identified by treating a multivalent recognition unit complex that has
CC      selective binding affinity for a WW domain, with many polypeptides and
CC      identifying those with selective affinity for the complex. Proteins
CC      containing WW domains are used for targeted drug screening, i.e. to
CC      identify potential modulators of specific WW domain interactions. The
CC      valency of the recognition unit is important in determining specificity
CC      of interaction with WW domains. In multivalent form specificity is
CC      relaxed, but not lost, so proteins containing WW domains similar, but not
CC      identical, to the sequence of the peptide's target WW can be detected,
CC      including new polypeptides
XX
SQ      Sequence 13 AA;

      Query Match                43.2%; Score 35; DB 2; Length 13;
      Best Local Similarity      71.4%; Pred. No. 1.9e+02;
      Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 FPPPPQE 12
      :|||||
Db      5 YPPPPPE 11

```

RESULT 43

ADB49201

ID ADB49201 standard; peptide; 13 AA.

XX

AC ADB49201;

XX

DT 04-DEC-2003 (first entry)

XX

DE Biotinylated peptide recognition unit #2.

XX

KW WW domain; drug candidate screening; drug discovery; drug modification;  
KW drug refinement; immunogen; WW binding protein; WW domain;  
KW peptide recognition unit.

XX

OS Synthetic.

XX

PN US2003077577-A1.

XX

PD 24-APR-2003.

XX

PF 28-JUN-2002; 2002US-00185050.

XX

PR 03-APR-1996; 96US-00630916.

PR 03-APR-1997; 97US-00826516.

XX

PA (PIRO/) PIROZZI G.

PA (KAYB/) KAY B K.

PA (FOWL/) FOWLKES D M.

XX

PI Pirozzi G, Kay BK, Fowlkes DM;

XX

DR WPI; 2003-635075/60.

XX

PT Novel purified polypeptide comprising WW domain, useful for drug  
PT discovery, modification and refinement, for discovering polypeptides  
PT involved in pharmacological activities, or as an immunogen to generate  
PT antibodies.

XX

PS Example; Fig 15A; 133pp; English.

XX

CC The invention describes a purified polypeptide (I) comprising a WW domain  
CC which has a sequence (S1) selected from 11 sequences fully defined in the  
CC specification, a sequence (S2) selected from 48 sequences fully defined  
CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725  
CC amino acids fully defined in the specification. (I) is useful for  
CC screening a potential drug candidate, by allowing (I) to come into  
CC contact with at least one recognition unit having a selective affinity  
CC for the WW domain in (I), in the presence of an amount of a potential  
CC drug candidate, such that (I) and the recognition unit are capable of  
CC interacting when brought into contact with one another in the absence of  
CC the drug candidate, and determining the effect, if any, of the presence  
CC of the amount of the drug candidate on the interaction of (I) with the  
CC recognition unit. (I) is useful for drug discovery, modification and  
CC refinement, for discovering polypeptides involved in pharmacological  
CC activities, or as an immunogen to generate antibodies. This is the amino  
CC acid sequence of a peptide recognition unit used to screen cDNA  
CC expression libraries for WW domain binding proteins.

XX

SQ Sequence 13 AA;

Query Match 43.2%; Score 35; DB 7; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPPPPQE 12

:|||| |

Db 5 YPPPPPE 11

#### RESULT 44

AAP10189

ID AAP10189 standard; protein; 15 AA.

XX

AC AAP10189;

XX

DT 10-AUG-1992 (first entry)

XX

DE Sequence of structure IV analogous to the C-terminal, 138-145 AA sequence  
DE of the beta subunits of human chorionic gonadotropin.

XX

KW Antigen; immunogen; contraceptive; fertility control.

XX

OS Homo sapiens.

XX

PN US4302386-A.

XX

PD 24-NOV-1981.

XX

PF 07-MAY-1973; 73US-00357892.

XX

PR 07-MAY-1973; 73US-00357892.

PR 16-OCT-1973; 73US-00406821.

PR 22-APR-1974; 74US-00462955.

PR 14-OCT-1975; 75US-00622031.

PR 25-AUG-1978; 78US-00936876.

PR 16-JAN-1980; 80US-00112628.

PR 20-NOV-1981; 81US-00323690.

PR 04-MAR-1983; 83US-00472190.

PR 15-JUL-1987; 87US-00073570.

PR 15-JUL-1987; 87US-00073769.

XX

PA (OHIS ) UNIV OHIO STATE.

XX

PI Stevens VC;

XX

DR WPI; 1981-92939D/50.

XX

PT Modified hormones and non-hormonal proteins - useful as antigens for  
PT admin. to produce antibodies for fertility control etc.

XX

PS Claim 13; Col 40; 25pp; English.

XX

CC The inventors claim modified hormones and non-hormonal proteins useful as  
CC antigens. 1-40 modifying gps. are pref. added per protein or hormone,

CC esp. 10-26 gps., partic. to FSH, HCG, LH, HPL, prolactin, gastrin,  
 CC angiotensin II, growth hormone, somatomedin, beta-sub units of HCG and  
 CC FSH. The polypeptide may be modified by addn. of at least one  
 CC diazosulphanilic acid, dinitrophenol, trinitrophenol, S-  
 CC acetomercaptosuccinic anhydride, (poly)tyrosine, (poly)alanine,  
 CC (poly)dextran or thyroglobulin, natural proteins, polymerised sugars,  
 CC serum protein or a virus. Typically, sucrose copolymerised with  
 CC epichlorohydrin is used for the modification, or diphtheria virus or  
 CC toxoid is used. Structure IV incorporates Cys component at the amino or N  
 CC -terminal which is associated with a Proline spacer sequence. These  
 CC spacers serve to position the sequence which follows physically distant  
 CC form the carrier-modifier. The latter sequence may be observed to  
 CC represent the 138th to 145th sequence of the beta subunit of HCG

XX

SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 1; Length 15;

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQET 13

|||| :|

Db 4 PPPPSDT 10

RESULT 45

AAP70999

ID AAP70999 standard; peptide; 15 AA.

XX

AC AAP70999;

XX

DT 05-APR-1991 (first entry)

XX

DE Sequence of fragment IV of human chorionic gonadotropin (HCG) beta  
 DE subunit.

XX

KW Fertility control; vaccine; Zollinger-Ellison syndrome; diabetes;  
 KW hypertension.

XX

OS Homo sapiens.

XX

PN CA1223206-A.

XX

PD 23-JUN-1987.

XX

PF 16-NOV-1982; 82CA-00415674.

XX

PR 20-NOV-1981; 81US-00323690.

PR 04-DEC-1985; 85US-00804462.

XX

PA (STEV/) STEVENS V C.

XX

PI Stevens VC;

XX

DR WPI; 1987-199114/29.

XX

PT Vaccines comprising modified polypeptide(s) - have mannide mono:oleate



PT and squalane or squalene as vehicle for enhanced efficacy.

XX

PS Disclosure; p14; 120pp; English.

XX

CC The vaccines comprise a modified peptide together with, as a vehicle, a  
CC mixt. of mannide mono-oleate with squalane and/or squalene. The  
CC unmodified peptide is typically a fragment of HCG, eg a specified  
CC polypeptide having 37 AAs. The fragment may be modified by being coupled  
CC to diphtheria toxoid, eg at 20-30 fragments per 100,000 daltons of toxoid.  
CC Cys residues may be linked through a disulphide bridge, and AA sequences  
CC may be attached through an AA spacer to a carrier. The vaccines may be  
CC used to treat Zollinger-Ellison syndrome, hypertension, diabetes and  
CC associated micro-and macro-vascular diseases, and endocrine or hormo

XX

SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 1; Length 15;

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPPQET 13

|||| :|

Db 4 PPPPSDT 10

#### RESULT 46

AAP80033

ID AAP80033 standard; protein; 15 AA.

XX

AC AAP80033;

XX

DT 12-NOV-1990 (first entry)

XX

DE Beta-human chorionic gonadotropin antigenically modified peptide (III).

XX

KW Human chorionic gonadotropin; isoimmunogen; thioester linkage;

KW halo-acetic acid; antibodies.

XX

OS Synthetic.

XX

PN US4762913-A.

XX

PD 09-AUG-1988.

XX

PF 15-JUL-1987; 87US-00073769.

XX

PR 07-MAY-1973; 73US-00357892.

PR 16-OCT-1973; 73US-00406821.

PR 22-APR-1974; 74US-00462955.

PR 14-OCT-1975; 75US-00622031.

PR 25-AUG-1978; 78US-00936876.

PR 16-JAN-1980; 80US-00112628.

PR 16-JAN-1981; 81US-00112628.

PR 20-NOV-1981; 81US-00323690.

PR 04-MAR-1983; 83US-00472190.

PR 02-NOV-1984; 84US-00667863.

PR 15-JUL-1987; 87US-00073570.

XX  
PA (OHIS ) UNIV OHIO STATE.  
XX  
PI Stevens VC;  
XX  
DR WPI; 1988-242553/34.  
XX  
PT Antigenic modification of polypeptide(s) - by forming thioether linkage  
PT with carrier via active ester of halo-acetic acid.  
XX  
PS Claim 6; Page 95; 57pp; English.  
XX  
CC The peptide is chemically modified outside the body of an animal so that  
CC when injected into the animal they produce more antibodies against the  
CC unmodified protein than would injection of the unmodified protein or  
CC fragment alone. The chemical modification may be accomplished by  
CC attaching the peptide to carriers such as, e.g. bacterial toxoids, or by  
CC polymerisation of the peptide. The product can be administered to animals  
CC for the purpose of contraception, abortion or treatment of hormone-  
CC related disease states and disorders, hormone associated carcinomas, and  
CC to boost the animals resistance to exogenous proteins, e.g. viral  
XX  
SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
||| :|  
Db 4 PPPPSDT 10

# RESULT 47

AAP91840

ID AAP91840 standard; peptide; 15 AA.

XX

AC AAP91840;

XX

DT 25-MAR-2003 (revised)

DT 06-MAR-1990 (first entry)

XX

DE Analogue of beta subunit of human chorionic gonadotropin.

XX

KW Human chorionic gonadotropin; beta-subunit; analogue; antibodies;

KW disulphide bridge.

XX

OS Homo sapiens.

XX

PN US4855285-A.

XX

PD 08-AUG-1989.

XX

PF 17-AUG-1987; 87US-00086401.

XX

PR 04-DEC-1985; 85US-00804642.

XX

PA (OHIS ) UNIV OHIO STATE.

XX

PI Stevens YC;

XX

DR WPI; 1989-285270/39.

XX

PT Controlling biological activity of chorionic gonadotropin - by  
PT administering a peptide comprising the 38-57 region coupled to material  
PT to evoke antibodies.

XX

PS Disclosure; Page 11; 82pp; English.

XX

CC The peptide incorporates an N-terminal Cys which is associated with a Pro  
CC spacer sequence. This spacer positions the sequence from the carrier/  
CC modifier. This latter sequence may be seen to present the 138-145 amino  
CC acid components of subunit structure of AAP91836. The peptide is coupled  
CC to a target material, eg poly(lysine), diphtheria or cholera toxoid,  
CC epichlorohydrin, etc, and used to form antibodies in primates which  
CC control chorionic gonadotropin activity. When the carrier is  
CC poly(lysine), a second polypeptide is added to increase antigenicity. The  
CC peptide can be used for contraception, abortion, to treat hormone-  
CC related diseases and disorders, hormone-associated carcinoma and to boost  
CC resistance to exogenous, eg viral, proteins. (Updated on 25-MAR-2003 to  
CC correct PF field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated  
CC on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 1; Length 15;

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQET 13

|||| :|

Db 4 PPPPSDT 10

#### RESULT 48

AAW39024

ID AAW39024 standard; peptide; 15 AA.

XX

AC AAW39024;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:423.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;  
KW PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US002298.

XX

PR 16-FEB-1996; 96US-00602999.

XX

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JE;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src tyrosine  
PT kinase(s) and to stimulate immune response by increasing production of  
PT certain lymphokine(s), e.g. interleukin-1.

XX

PS Claim 22; Page 93; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology  
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain  
CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
CC can be used in the method to identify inhibitors of their binding to  
CC their respective SH3 domains, which could be used to modulate the  
CC pharmacological activity of proteins or polypeptide containing the SH3  
CC domain. The peptides can also be used to activate Src or Src-related  
CC protein tyrosine kinases, to stimulate the immune response by increasing  
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
CC and interleukin-1, or to deliver a conjugated molecule to certain  
CC cellular compartments containing Src or Src related proteins

XX

SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 2; Length 15;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQE 12

||||:

Db 8 PPPPEE 13

RESULT 49

AAW38952

ID AAW38952 standard; peptide; 15 AA.

XX

AC AAW38952;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:349.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;  
KW PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US002298.

XX

PR 16-FEB-1996; 96US-00602999.

XX

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JE;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src tyrosine  
PT kinase(s) and to stimulate immune response by increasing production of  
PT certain lymphokine(s), e.g. interleukin-1.

XX

PS Claim 22; Page 91; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology  
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain  
CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
CC can be used in the method to identify inhibitors of their binding to  
CC their respective SH3 domains, which could be used to modulate the  
CC pharmacological activity of proteins or polypeptide containing the SH3  
CC domain. The peptides can also be used to activate Src or Src-related  
CC protein tyrosine kinases, to stimulate the immune response by increasing  
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
CC and interleukin-1, or to deliver a conjugated molecule to certain  
CC cellular compartments containing Src or Src related proteins

XX

SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 2; Length 15;

Best Local Similarity 54.5%; Pred. No. 2.2e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMKFPPPPQE 12

| : |||||:

Db 1 LPSREPPPPQK 11

RESULT 50

AAW37268

ID AAW37268 standard; peptide; 15 AA.

XX

AC AAW37268;

XX

DT 08-JUN-1998 (first entry)

XX

DE Peptide derived from amino acids 138-145 of the beta subunit of hCG.

XX

KW Beta subunit; chorionic gonadotropin; hCG; CG; luteinising hormone; LH;

KW immunogenic carrier; conjugate; immunisation; treatment;

KW neoplastic tumour; carcinoma tumour.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN US5698201-A.

XX

PD 16-DEC-1997.

XX

PF 06-JUN-1995; 95US-00468716.

XX

PR 07-MAY-1973; 73US-00357892.

PR 16-OCT-1973; 73US-00406821.

PR 22-APR-1974; 74US-00462955.

PR 14-OCT-1975; 75US-00622031.

PR 25-AUG-1978; 78US-00936876.

PR 16-JAN-1981; 81US-00112628.

PR 20-NOV-1981; 81US-00323690.

PR 04-MAR-1983; 83US-00472190.

PR 02-NOV-1984; 84US-00667863.

PR 15-JUL-1987; 87US-00073748.

PR 17-FEB-1989; 89US-00311331.

PR 26-AUG-1992; 92US-00935331.

XX

PA (OHIS ) UNIV OHIO STATE.

XX

PI Stevens VC;

XX

DR WPI; 1998-051434/05.

XX

PT Treatment of tumours expressing chorionic gonadotropin - by immunisation

PT with conjugate of CG polypeptide and immunogenic carrier.

XX

PS Disclosure; Col 19; 57pp; English.

XX

CC The present sequence is derived from amino acids 138-145 of the beta  
CC subunit of human chorionic gonadotropin (hCG). The peptide incorporates a  
CC Cys component at the amino terminal which is associated with a proline  
CC spacer sequence. These spacers serve to position the sequence which  
CC follows so that it is physically distant from the carrier. A large part  
CC of the beta subunit of hCG is almost identical to the corresponding beta  
CC subunit of luteinising hormone (LH). The present sequence is derived from  
CC a portion of the beta subunit that is not common to LH. The present  
CC sequence is coupled to an immunogenic carrier (biologically foreign to  
CC the mammal) to create a conjugate. This conjugate is used to immunise a

CC mammal and thus treat a neoplastic tumour expressing CG. The CG  
CC polypeptide is nonimmunogenic to the animal but the conjugate induces  
CC formation of antibodies that are reactive with CG expressed by the  
CC tumour. The method is especially useful for treating carcinoma tumours in  
CC humans  
XX  
SQ Sequence 15 AA;

Query Match 43.2%; Score 35; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
| | | | : |  
Db 4 PPPPSDT 10

Search completed: July 4, 2004, 04:40:54  
Job time : 39.1493 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 9.40299 Seconds  
(without alignments)  
82.356 Million cell updates/sec

Title: US-09-641-802-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	81	100.0	15	4	US-09-641-803-7	Sequence 7, Appli
2	37	45.7	18	3	US-08-630-916A-109	Sequence 109, App
3	37	45.7	18	3	US-08-602-999A-305	Sequence 305, App
4	37	45.7	18	4	US-08-630-915A-165	Sequence 165, App
5	37	45.7	18	4	US-09-500-124-305	Sequence 305, App
6	35	43.2	10	2	US-08-968-676-19	Sequence 19, Appl
7	35	43.2	12	2	US-08-968-676-161	Sequence 161, App
8	35	43.2	13	3	US-08-630-916A-7	Sequence 7, Appli
9	35	43.2	15	3	US-08-602-999A-349	Sequence 349, App
10	35	43.2	15	3	US-08-602-999A-423	Sequence 423, App
11	35	43.2	15	4	US-09-500-124-349	Sequence 349, App



12	35	43.2	15	4	US-09-500-124-423	Sequence 423, App
13	35	43.2	16	2	US-08-968-676-1	Sequence 1, Appli
14	35	43.2	16	4	US-09-396-813-1	Sequence 1, Appli
15	34	42.0	9	2	US-08-968-676-160	Sequence 160, App
16	34	42.0	10	2	US-08-968-676-18	Sequence 18, Appl
17	34	42.0	10	6	5252466-18	Patent No. 5252466
18	34	42.0	15	3	US-08-630-916A-55	Sequence 55, Appl
19	34	42.0	15	3	US-08-602-999A-339	Sequence 339, App
20	34	42.0	15	3	US-08-602-999A-405	Sequence 405, App
21	34	42.0	15	4	US-09-500-124-339	Sequence 339, App
22	34	42.0	15	4	US-09-500-124-405	Sequence 405, App
23	34	42.0	16	1	US-08-188-223-7	Sequence 7, Appli
24	34	42.0	16	2	US-08-844-312-8	Sequence 8, Appli
25	34	42.0	16	2	US-08-844-312-10	Sequence 10, Appl
26	34	42.0	16	3	US-08-968-466-7	Sequence 7, Appli
27	34	42.0	16	4	US-08-478-546B-7	Sequence 7, Appli
28	34	42.0	17	4	US-09-060-299-403	Sequence 403, App
29	34	42.0	17	4	US-09-402-923A-403	Sequence 403, App
30	33	40.7	7	4	US-09-641-803-14	Sequence 14, Appl
31	33	40.7	11	4	US-09-547-693-135	Sequence 135, App
32	33	40.7	11	4	US-09-547-693-199	Sequence 199, App
33	33	40.7	12	3	US-08-630-916A-52	Sequence 52, Appl
34	33	40.7	12	3	US-08-630-916A-88	Sequence 88, Appl
35	33	40.7	12	4	US-08-630-915A-144	Sequence 144, App
36	33	40.7	15	1	US-08-302-771-1	Sequence 1, Appli
37	33	40.7	15	3	US-08-602-999A-367	Sequence 367, App
38	33	40.7	15	3	US-08-602-999A-373	Sequence 373, App
39	33	40.7	15	3	US-08-602-999A-439	Sequence 439, App
40	33	40.7	15	4	US-09-500-124-367	Sequence 367, App
41	33	40.7	15	4	US-09-500-124-373	Sequence 373, App
42	33	40.7	15	4	US-09-500-124-439	Sequence 439, App
43	33	40.7	16	3	US-08-630-916A-11	Sequence 11, Appl
44	33	40.7	17	3	US-08-602-999A-336	Sequence 336, App
45	33	40.7	17	4	US-09-500-124-336	Sequence 336, App
46	32	39.5	15	3	US-08-976-255-20	Sequence 20, Appl
47	32	39.5	18	1	US-08-279-058B-20	Sequence 20, Appl
48	32	39.5	18	4	US-08-828-323-20	Sequence 20, Appl
49	31	38.3	8	4	US-09-343-011B-9	Sequence 9, Appli
50	31	38.3	9	4	US-09-295-996B-29	Sequence 29, Appl
51	31	38.3	9	4	US-09-295-846B-32	Sequence 32, Appl
52	31	38.3	9	4	US-09-551-737C-32	Sequence 32, Appl
53	31	38.3	9	4	US-09-551-738B-29	Sequence 29, Appl
54	31	38.3	10	1	US-08-230-047-11	Sequence 11, Appl
55	31	38.3	10	2	US-08-968-676-162	Sequence 162, App
56	31	38.3	11	1	US-08-336-343A-26	Sequence 26, Appl
57	31	38.3	11	3	US-08-652-877-23	Sequence 23, Appl
58	31	38.3	11	3	US-08-476-515A-23	Sequence 23, Appl
59	31	38.3	12	3	US-08-602-999A-268	Sequence 268, App
60	31	38.3	12	4	US-09-460-384-25	Sequence 25, Appl
61	31	38.3	12	4	US-09-500-124-268	Sequence 268, App
62	31	38.3	12	4	US-09-845-917A-22	Sequence 22, Appl
63	31	38.3	12	4	US-09-428-082B-312	Sequence 312, App
64	31	38.3	12	4	US-09-428-082B-313	Sequence 313, App
65	31	38.3	13	4	US-09-460-384-26	Sequence 26, Appl
66	31	38.3	14	3	US-08-630-916A-56	Sequence 56, Appl
67	31	38.3	15	3	US-08-602-999A-298	Sequence 298, App
68	31	38.3	15	3	US-08-602-999A-352	Sequence 352, App

69	31	38.3	15	3	US-08-602-999A-354	Sequence 354, App
70	31	38.3	15	3	US-08-602-999A-377	Sequence 377, App
71	31	38.3	15	4	US-09-500-124-298	Sequence 298, App
72	31	38.3	15	4	US-09-500-124-352	Sequence 352, App
73	31	38.3	15	4	US-09-500-124-354	Sequence 354, App
74	31	38.3	15	4	US-09-500-124-377	Sequence 377, App
75	31	38.3	16	1	US-08-064-400B-1	Sequence 1, Appli
76	31	38.3	16	1	US-08-477-509B-17	Sequence 17, Appl
77	31	38.3	16	2	US-08-968-676-2	Sequence 2, Appli
78	31	38.3	16	2	US-08-844-312-11	Sequence 11, Appl
79	31	38.3	16	3	US-08-630-916A-107	Sequence 107, App
80	31	38.3	16	3	US-08-482-085B-17	Sequence 17, Appl
81	31	38.3	16	3	US-08-602-999A-344	Sequence 344, App
82	31	38.3	16	3	US-08-602-999A-422	Sequence 422, App
83	31	38.3	16	4	US-08-630-915A-163	Sequence 163, App
84	31	38.3	16	4	US-09-444-791A-17	Sequence 17, Appl
85	31	38.3	16	4	US-09-396-813-2	Sequence 2, Appli
86	31	38.3	16	4	US-09-500-124-344	Sequence 344, App
87	31	38.3	16	4	US-09-500-124-422	Sequence 422, App
88	31	38.3	16	5	PCT-US94-05617-1	Sequence 1, Appli
89	31	38.3	17	3	US-08-602-999A-380	Sequence 380, App
90	31	38.3	17	3	US-08-602-999A-383	Sequence 383, App
91	31	38.3	17	4	US-09-500-124-380	Sequence 380, App
92	31	38.3	17	4	US-09-500-124-383	Sequence 383, App
93	31	38.3	18	4	US-09-641-803-22	Sequence 22, Appl
94	30	37.0	10	4	US-08-983-157B-19	Sequence 19, Appl
95	30	37.0	10	4	US-08-983-157B-20	Sequence 20, Appl
96	30	37.0	12	2	US-08-556-597-138	Sequence 138, App
97	30	37.0	12	3	US-08-602-999A-256	Sequence 256, App
98	30	37.0	12	4	US-09-500-124-256	Sequence 256, App
99	30	37.0	14	4	US-08-837-199A-29	Sequence 29, Appl
100	30	37.0	15	3	US-08-602-999A-382	Sequence 382, App

#### ALIGNMENTS

##### RESULT 1

US-09-641-803-7

; Sequence 7, Application US/09641803

; Patent No. 6500798

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/09/641,803

; CURRENT FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-7

Query Match 100.0%; Score 81; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15  
| | | | | | | | | | | | | | |  
Db 1 VLEMKFPPPPQETVT 15

RESULT 2

US-08-630-916A-109

; Sequence 109, Application US/08630916A

; Patent No. 6011137

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; APPLICANT: Kay, Brian K.

; APPLICANT: Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,916A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-203

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741

; INFORMATION FOR SEQ ID NO: 109:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-630-916A-109

Query Match 45.7%; Score 37; DB 3; Length 18;  
Best Local Similarity 60.0%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
| ||||| :  
Db 7 EPDFPPPPPD 16

RESULT 3

US-08-602-999A-305

; Sequence 305, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 305:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-602-999A-305

Query Match 45.7%; Score 37; DB 3; Length 18;  
Best Local Similarity 55.6%; Pred. No. 15;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPPQETV 14  
||||| : :  
Db 7 FPPPPYQPI 15

RESULT 4

US-08-630-915A-165

; Sequence 165, Application US/08630915A

; Patent No. 6309820

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: HOFFMAN, No. 6309820h

; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: McCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; TITLE OF INVENTION: USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 165:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-630-915A-165

Query Match 45.7%; Score 37; DB 4; Length 18;  
Best Local Similarity 60.0%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
| |||| :  
Db 7 EPDFPPPPPD 16

RESULT 5

US-09-500-124-305

; Sequence 305, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 305:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-09-500-124-305

Query Match 45.7%; Score 37; DB 4; Length 18;  
Best Local Similarity 55.6%; Pred. No. 15;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPPQETV 14  
||||| : :  
Db 7 FPPPPYQPI 15

RESULT 6

US-08-968-676-19

; Sequence 19, Application US/08968676  
; Patent No. 5919639  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,676  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-968-676-19

Query Match 43.2%; Score 35; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 16;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11  
| || | ||:  
Db 1 LRMKLPKPPK 10

RESULT 7

US-08-968-676-161

; Sequence 161, Application US/08968676

; Patent No. 5919639

; GENERAL INFORMATION:

; APPLICANT: Humphreys, Robert E

; APPLICANT: Adams, Sharlene

; APPLICANT: Xu, Minzhen

; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN

; NUMBER OF SEQUENCES: 165

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999

; CITY: York Harbor

; STATE: ME

; COUNTRY: USA

; ZIP: 03911

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/968,676

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Farrell, Kevin M

; REGISTRATION NUMBER: 35,505

; REFERENCE/DOCKET NUMBER: REH-9601

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (207) 363-0558

; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 161:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-968-676-161

Query Match 43.2%; Score 35; DB 2; Length 12;

Best Local Similarity 60.0%; Pred. No. 20;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11  
| || | ||:  
Db 1 LRMKLPKPPK 10

RESULT 8



US-08-630-916A-7  
; Sequence 7, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-7

Query Match 43.2%; Score 35; DB 3; Length 13;  
Best Local Similarity 71.4%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPPPPQE 12  
:|||||  
Db 5 YPPPPPE 11

RESULT 9  
US-08-602-999A-349  
; Sequence 349, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-349

```

```

Query Match          43.2%; Score 35; DB 3; Length 15;
Best Local Similarity 54.5%; Pred. No. 25;
Matches      6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 LEMKFPPPPQE 12
        | : ||||:
Db      1 LPSREPPPPQK 11

```

```

RESULT 10
US-08-602-999A-423
; Sequence 423, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

```

```

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-423

```

```

Query Match          43.2%; Score 35; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 25;
Matches      5; Conservative 1; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      7 PPPPQE 12
        ||||:|
Db      8 PPPPEE 13

```

```

RESULT 11
US-09-500-124-349
; Sequence 349, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.

```

```

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-349

```

```

Query Match          43.2%; Score 35; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 25;
Matches      6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 LEMKFPPPPQE 12
        | : ||||:
Db      1 LPSREPPPPQK 11

```

```

RESULT 12
US-09-500-124-423
; Sequence 423, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:

```

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-423

```

```

Query Match          43.2%; Score 35; DB 4; Length 15;
Best Local Similarity 83.3%; Pred. No. 25;
Matches      5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 PPPPQE 12
        ||||:|
Db      8 PPPPEE 13

```

```

RESULT 13
US-08-968-676-1
; Sequence 1, Application US/08968676

```

```

; Patent No. 5919639
; GENERAL INFORMATION:
;   APPLICANT:  Humphreys, Robert E
;   APPLICANT:  Adams, Sharlene
;   APPLICANT:  Xu, Minzhen
;   TITLE OF INVENTION:  IMMUNOTHERAPY BY MODULATION OF ANTIGEN
;   NUMBER OF SEQUENCES:  165
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Kevin M. Farrell, P.C.
;     STREET:    P.O. Box 999
;     CITY:      York Harbor
;     STATE:     ME
;     COUNTRY:   USA
;     ZIP:       03911
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/968,676
;     FILING DATE:
;     CLASSIFICATION:     424
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Farrell, Kevin M
;     REGISTRATION NUMBER:  35,505
;     REFERENCE/DOCKET NUMBER:  REH-9601
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (207) 363-0558
;     TELEFAX:   (207) 363-0528
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-968-676-1

```

```

Query Match          43.2%;  Score 35;  DB 2;  Length 16;
Best Local Similarity 60.0%;  Pred. No. 27;
Matches      6;  Conservative      1;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      2 LEMKFPPPPQ 11
        | | | | |
Db      1 LRMKLPKPPK 10

```

RESULT 14

US-09-396-813-1

```

; Sequence 1, Application US/09396813
; Patent No. 6432409

```

; GENERAL INFORMATION:

```

; APPLICANT:  Humphreys, Robert E.
; APPLICANT:  Adams, Sharlene
; APPLICANT:  Xu, Minzhen
; TITLE OF INVENTION:  HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE

```

; FILE REFERENCE: REH2007  
; CURRENT APPLICATION NUMBER: US/09/396,813  
; CURRENT FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-396-813-1

Query Match 43.2%; Score 35; DB 4; Length 16;  
Best Local Similarity 60.0%; Pred. No. 27;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11  
| || | ||:  
Db 1 LRMKLPKPPK 10

RESULT 15

US-08-968-676-160

; Sequence 160, Application US/08968676  
; Patent No. 5919639  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/968,676  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 160:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-968-676-160

Query Match 42.0%; Score 34; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPP 10  
| | | | |  
Db 1 LRMKLPKPP 9

RESULT 16

US-08-968-676-18

; Sequence 18, Application US/08968676  
; Patent No. 5919639

; GENERAL INFORMATION:

; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME  
; COUNTRY: USA  
; ZIP: 03911

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/968,676  
; FILING DATE:  
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Farrell, Kevin M  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: REH-9601

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-968-676-18

Query Match 42.0%; Score 34; DB 2; Length 10;



Best Local Similarity 66.7%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPP 10  
| | | | |  
Db 1 LRMKLPKPP 9

RESULT 17

5252466-18

; Patent No. 5252466

; APPLICANT: CRONAN, JOHN E.

; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN

; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND

; PURIFYING THEM

; NUMBER OF SEQUENCES: 24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/525,568

; FILING DATE: 18-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 354,266

; FILING DATE: 19-MAY-1989

; SEQ ID NO:18:

; LENGTH: 10

5252466-18

Query Match 42.0%; Score 34; DB 6; Length 10;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQETV 14  
| | | | |  
Db 3 PPPPPGTV 10

RESULT 18

US-08-630-916A-55

; Sequence 55, Application US/08630916A

; Patent No. 6011137

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; APPLICANT: Kay, Brian K.

; APPLICANT: Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/630,916A
;   FILING DATE:  03-APR-1996
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  MISROCK, S. LESLIE
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-203
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 896-8864/9741
;   INFORMATION FOR SEQ ID NO:  55:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  15 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-08-630-916A-55

```

```

Query Match          42.0%;  Score 34;  DB 3;  Length 15;
Best Local Similarity 75.0%;  Pred. No. 35;
Matches      6;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

```

```

Qy      7 PPPPQETV 14
        ||||  ||
Db      4 PPPPPYTV 11

```

# RESULT 19

US-08-602-999A-339

```

; Sequence 339, Application US/08602999A
; Patent No. 6184205

```

## GENERAL INFORMATION:

```

;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  RIDER, James E.
;   TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION:  ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-339

```

```

Query Match          42.0%; Score 34; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 35;
Matches      5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 PPPPQE 12
        |||||:
Db      6 PPPPQK 11

```

# RESULT 20

```

US-08-602-999A-405
; Sequence 405, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-405

```

```

Query Match          42.0%; Score 34; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 35;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      5 KFPPPPQ 11
        | |||||
Db      4 KPPPPQ 10

```

# RESULT 21

```

US-09-500-124-339
; Sequence 339, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 339:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-339

Query Match 42.0%; Score 34; DB 4; Length 15;  
Best Local Similarity 83.3%; Pred. No. 35;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
| | | | :  
Db 6 PPPPQK 11

RESULT 22

US-09-500-124-405

; Sequence 405, Application US/09500124  
; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-405

```

```

Query Match          42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 85.7%; Pred. No. 35;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      5 KFPPPPQ 11
        | |||||
Db      4 KPPPPPPQ 10

```

# RESULT 23

US-08-188-223-7

```

; Sequence 7, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223

```

```

; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..16
; OTHER INFORMATION: /note= "immunomimic"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /label= GlyNH2
; OTHER INFORMATION: /note= "glycinamide"
US-08-188-223-7

```

```

Query Match          42.0%; Score 34; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 38;
Matches      5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 PPPPQE 12
        ||||:|
Db      2 PPPPRE 7

```

#### RESULT 24

US-08-844-312-8

```

; Sequence 8, Application US/08844312
; Patent No. 5948639

```

#### GENERAL INFORMATION:

```

; APPLICANT: Carlos J. Gimeno and Dean A. Falb
; TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway

```

#### Genes

```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,312
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-844-312-8

```

```

Query Match          42.0%; Score 34; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 38;
Matches      5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      3 EMKFPPPP 10
        |:: |||
Db      4 ELESPPPP 11

```

# RESULT 25

US-08-844-312-10

; Sequence 10, Application US/08844312

; Patent No. 5948639

; GENERAL INFORMATION:

; APPLICANT: Carlos J. Gimeno and Dean A. Falb

; TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway

Genes

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:



```

; APPLICATION NUMBER: US/08/844,312
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-844-312-10

```

```

Query Match          42.0%; Score 34; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 38;
Matches      5; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      3 EMKFPPPP 10
        |:: ||||
Db      4 ELESPPPP 11

```

RESULT 26

US-08-968-466-7

```

; Sequence 7, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME:  Drivas Esq., Dimitrios T.
;   REGISTRATION NUMBER:  32,218
;   REFERENCE/DOCKET NUMBER:  1102865-300
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  212-819-8286
;   TELEFAX:  212-354-8113
; INFORMATION FOR SEQ ID NO:  7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  16 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
; MOLECULE TYPE:  peptide
; HYPOTHETICAL:  YES
; FEATURE:
;   NAME/KEY:  Region
;   LOCATION:  1..6
;   OTHER INFORMATION:  /note= "spacer"
; FEATURE:
;   NAME/KEY:  Region
;   LOCATION:  7..16
;   OTHER INFORMATION:  /note= "immunomimic"
; FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  16
;   OTHER INFORMATION:  /label= GlyNH2
;   OTHER INFORMATION:  /note= "glycinamide"
US-08-968-466-7

```

```

Query Match          42.0%;  Score 34;  DB 3;  Length 16;
Best Local Similarity 83.3%;  Pred. No. 38;
Matches      5;  Conservative    1;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      7 PPPPQE 12
        ||||:|
Db      2 PPPPRE 7

```

# RESULT 27

US-08-478-546B-7

```

; Sequence 7, Application US/08478546B
; Patent No. 6303123

```

## GENERAL INFORMATION:

```

; APPLICANT:  Grimes, Stephen
; APPLICANT:  Scibienski, Robert
; TITLE OF INVENTION:  Methods for the Treatment of Hormone-Dependent
; TITLE OF INVENTION:  Tumors with Immunogens against Gonadotropin Releasing
Hormone

```

```

; NUMBER OF SEQUENCES:  11
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Dimitrios T. Drivas, Esq.
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  NY
;   COUNTRY:  USA
;   ZIP:  10036-2787
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..16
; OTHER INFORMATION: /note= "immunomimic"
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 16
; OTHER INFORMATION: /note= Xaa
; OTHER INFORMATION: /note= "amidated glycine"
US-08-478-546B-7

```

```

Query Match          42.0%; Score 34; DB 4; Length 16;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 PPPPQE 12
        ||||:|
Db      2 PPPPRE 7

```

```

RESULT 28
US-09-060-299-403
; Sequence 403, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T

```

```

; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137e1 Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 403:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-060-299-403

```

```

Query Match          42.0%; Score 34; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 40;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 FPPPP 10
        |||||
Db      6 FPPPP 10

```

```

RESULT 29
US-09-402-923A-403
; Sequence 403, Application US/09402923A
; Patent No. 6555654

```

```

; GENERAL INFORMATION:
;   APPLICANT: Todd, John A
;               Hess, John W
;               Caskey, Charles T
;               Cox, Roger D
;               Gerhold, David
;               Hammond, Holly
;               Hey, Patricia
;               Kawaguchi, Yoshihiko
;               Merriman, Tony R
;               Metzker, Michael L
;   TITLE OF INVENTION: No. 6555654e1 LDL-Receptor
;   NUMBER OF SEQUENCES: 455
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Nixon and Vanderhye
;       STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
;       CITY: Arlington
;       STATE: Virginia
;       COUNTRY: US
;       ZIP: VA 22201-4714
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/402,923A
;       FILING DATE: 14-Feb-2001
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: PCT/GB98/01102
;       FILING DATE: 15-APR-1998
;       APPLICATION NUMBER: US 60/043,553
;       FILING DATE: 15-APR-1997
;       APPLICATION NUMBER: US 60/048,740
;       FILING DATE: 05-JUN-1997
;   ATTORNEY/AGENT INFORMATION:
;       NAME: B.J.Sadoff
;       REGISTRATION NUMBER: 36,663
;       REFERENCE/DOCKET NUMBER: 620-81
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (703)816-4091
;       TELEFAX: (703)816-4100
;   INFORMATION FOR SEQ ID NO: 403:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 17 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-09-402-923A-403

```

```

Query Match          42.0%; Score 34; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 40;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 FPPPP 10
        |||||
Db      6 FPPPP 10

```

RESULT 30

US-09-641-803-14

; Sequence 14, Application US/09641803  
 ; Patent No. 6500798  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/09/641,803  
 ; CURRENT FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 14  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide

US-09-641-803-14

Query Match 40.7%; Score 33; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
 |||||  
 Db 2 PPPPQ 6

RESULT 31

US-09-547-693-135

; Sequence 135, Application US/09547693  
 ; Patent No. 6639050  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieliszewski, Marcia  
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other  
 Hydroxyproline-Rich  
 ; TITLE OF INVENTION: Glycoproteins  
 ; FILE REFERENCE: OHU-04089  
 ; CURRENT APPLICATION NUMBER: US/09/547,693  
 ; CURRENT FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 236  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 135  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Acacia senegal  
 ; FEATURE:  
 ; NAME/KEY: SITE

; LOCATION: (1)..(4)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
US-09-547-693-135

Query Match 40.7%; Score 33; DB 4; Length 11;  
Best Local Similarity 71.4%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
| | | | |  
Db 1 PPPPSST 7

RESULT 32

US-09-547-693-199

; Sequence 199, Application US/09547693  
; Patent No. 6639050  
; GENERAL INFORMATION:  
; APPLICANT: Kieliszewski, Marcia  
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other  
Hydroxyproline-Rich  
; TITLE OF INVENTION: Glycoproteins  
; FILE REFERENCE: OHU-04089  
; CURRENT APPLICATION NUMBER: US/09/547,693  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 236  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 199  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Acacia senegal  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(4)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
US-09-547-693-199

Query Match 40.7%; Score 33; DB 4; Length 11;  
Best Local Similarity 71.4%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
| | | | |  
Db 1 PPPPSST 7

RESULT 33

US-08-630-916A-52

; Sequence 52, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME

```

;   NUMBER OF SEQUENCES: 124
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: United States
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/630,916A
;     FILING DATE: 03-APR-1996
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: MISROCK, S. LESLIE
;     REGISTRATION NUMBER: 18,872
;     REFERENCE/DOCKET NUMBER: 1101-203
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 790-9090
;     TELEFAX: (212) 896-8864/9741
;   INFORMATION FOR SEQ ID NO: 52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 12 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: unknown
;     MOLECULE TYPE: peptide
US-08-630-916A-52

```

```

Query Match          40.7%; Score 33; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. No. 40;
Matches      4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 FPPPPQ 11
        :| | | :
Db      5 YPPPPPE 10

```

#### RESULT 34

US-08-630-916A-88

; Sequence 88, Application US/08630916A

; Patent No. 6011137

#### ; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; APPLICANT: Kay, Brian K.

; APPLICANT: Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME

; NUMBER OF SEQUENCES: 124

#### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas



```

;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  United States
;   ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/630,916A
;   FILING DATE:  03-APR-1996
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  MISROCK, S. LESLIE
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-203
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 896-8864/9741
;   INFORMATION FOR SEQ ID NO:  88:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  12 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-08-630-916A-88

```

```

Query Match          40.7%;  Score 33;  DB 3;  Length 12;
Best Local Similarity 66.7%;  Pred. No. 40;
Matches      4;  Conservative    2;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      6 FPPPPQ 11
        :||||:
Db      5 YPPPE 10

```

# RESULT 35

```

US-08-630-915A-144
; Sequence 144, Application US/08630915A
; Patent No. 6309820
;   GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  HOFFMAN, No. 6309820h
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  McCONNELL, Stephen J.
;   TITLE OF INVENTION:  POLYPEPTIDES HAVING A FUNCTIONAL
;   TITLE OF INVENTION:  DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
;   TITLE OF INVENTION:  USING SAME
;   NUMBER OF SEQUENCES:  227
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds LLP
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York

```

```

; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-144

```

```

Query Match          40.7%; Score 33; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 40;
Matches      4; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 FPPPPQ 11
        :||||:
Db      5 YPPPE 10

```

# RESULT 36

US-08-302-771-1

```

; Sequence 1, Application US/08302771
; Patent No. 5599541
; GENERAL INFORMATION:
; APPLICANT: MARCHAL, GILLES
; APPLICANT: ROMAIN, FELIX
; TITLE OF INVENTION: PEPTIDE SEQUENCE CAPABLE OF INDUCING
; TITLE OF INVENTION: A
; TITLE OF INVENTION: DELAYED-TYPE HYPERSENSITIVITY REACTION IN THE PRESENCE
; TITLE OF INVENTION: OF
; TITLE OF INVENTION: LIVING BACTERIA OF THE MYCOBACTERIUM TUBERCULOSIS
; TITLE OF INVENTION: COMPLEX
; TITLE OF INVENTION: AND ITS APPLICATIONS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON

```

```

; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,771
; FILING DATE: OCTOBER 17, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92 03 286
; FILING DATE: 19-MAR-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
US-08-302-771-1

```

```

Query Match          40.7%; Score 33; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 PPPPQ 11
        |||||
Db      7 PPPPQ 11

```

```

RESULT 37
US-08-602-999A-367
; Sequence 367, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.

```

; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/602,999A  
 ; FILING DATE: 16-FEB-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 367:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 US-08-602-999A-367

Query Match 40.7%; Score 33; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
 |||||  
 Db 9 PPPPQ 13

RESULT 38  
 US-08-602-999A-373  
 ; Sequence 373, Application US/08602999A  
 ; Patent No. 6184205  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.

```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-373

```

```

Query Match          40.7%; Score 33; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 PPPPQ 11
        |||||
Db      6 PPPPQ 10

```

```

RESULT 39
US-08-602-999A-439
; Sequence 439, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

```

```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 439:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-439

```

```

Query Match          40.7%; Score 33; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      7 PPPPQ 11
        |||||
Db      6 PPPPQ 10

```

```

RESULT 40
US-09-500-124-367
; Sequence 367, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.

```

```

; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/500,124
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/602,999
;   FILING DATE:  16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  367:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  15 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-09-500-124-367

```

```

Query Match          40.7%;  Score 33;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 50;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      7 PPPPQ 11
        |||||
Db      9 PPPPQ 13

```

```

RESULT 41
US-09-500-124-373
; Sequence 373, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.

```

```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-373

```

```

Query Match          40.7%; Score 33; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 50;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 PPPPQ 11
        |||||
Db      6 PPPPQ 10

```

```

RESULT 42
US-09-500-124-439
; Sequence 439, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

```



; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/500,124  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 439:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 US-09-500-124-439

Query Match 40.7%; Score 33; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
 |||||  
 Db 6 PPPPQ 10

RESULT 43  
 US-08-630-916A-11  
 ; Sequence 11, Application US/08630916A  
 ; Patent No. 6011137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pirozzi, Gregorio

```

; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-11

```

```

Query Match          40.7%; Score 33; DB 3; Length 16;
Best Local Similarity 66.7%; Pred. No. 53;
Matches      4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 FPPPPQ 11
        :|||:
Db      9 YPPPE 14

```

```

RESULT 44
US-08-602-999A-336
; Sequence 336, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.

```

```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-336

```

```

Query Match          40.7%; Score 33; DB 3; Length 17;
Best Local Similarity 83.3%; Pred. No. 57;
Matches      5; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      5 KFPPPP 10
        | |||
Db      5 KMPPPP 10

```

```

RESULT 45
US-09-500-124-336
; Sequence 336, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

```

```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-336

```

```

Query Match          40.7%; Score 33; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 57;
Matches    5; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

```

```

Qy      5 KFPPPP 10
        | |||
Db      5 KMPPPP 10

```

RESULT 46

```

US-08-976-255-20
; Sequence 20, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-976-255-20

```

```

Query Match          39.5%; Score 32; DB 3; Length 15;
Best Local Similarity 45.5%; Pred. No. 71;
Matches      5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      3 EMKFPPPPQET 13
        |: | || ::|
Db      3 EIDFTPPAEDT 13

```

```

RESULT 47
US-08-279-058B-20
; Sequence 20, Application US/08279058B
; Patent No. 5668004
; GENERAL INFORMATION:
; APPLICANT: Michael E. O'Donnell
; TITLE OF INVENTION: DNA POLYMERASE III
; TITLE OF INVENTION: HOLOENZYME
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Yahwak & Associates  
 ; STREET: 25 Skytop Drive  
 ; CITY: Trumbull  
 ; STATE: Connecticut  
 ; COUNTRY: USA  
 ; ZIP: 06611  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Macintosh  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Microsoft Word 4.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/279,058B  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: George M. Yahwak  
 ; REGISTRATION NUMBER: 26,824  
 ; REFERENCE/DOCKET NUMBER: CRF D-1056CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (203)268-1951  
 ; TELEFAX: (203)268-1951  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-279-058B-20

Query Match 39.5%; Score 32; DB 1; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 86;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPPPQETVT 15  
 ||| | ||  
 Db 6 PPPEQYAVT 14

RESULT 48  
 US-08-828-323-20  
 ; Sequence 20, Application US/08828323A  
 ; Patent No. 6413753  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Donnell, Michael  
 ; TITLE OF INVENTION: DNA POLYMERASE III HOLOENZYME  
 ; FILE REFERENCE: 19603/10214  
 ; CURRENT APPLICATION NUMBER: US/08/828,323A  
 ; CURRENT FILING DATE: 1997-03-28  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 20  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 US-08-828-323-20

Query Match 39.5%; Score 32; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 86;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPPPQETVT 15  
||| | ||  
Db 6 PPPEQYAVT 14

RESULT 49

US-09-343-011B-9

; Sequence 9, Application US/09343011B  
; Patent No. 6300473  
; GENERAL INFORMATION:  
; APPLICANT: Stephane Richard  
; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL  
; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS  
; FILE REFERENCE: A32561  
; CURRENT APPLICATION NUMBER: US/09/343,011B  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: CA 2265271  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-343-011B-9

Query Match 38.3%; Score 31; DB 4; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
|||| |  
Db 2 PPPPPPT 8

RESULT 50

US-09-295-996B-29

; Sequence 29, Application US/09295996B  
; Patent No. 6413530  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: PESTICIDAL PEPTIDES  
; FILE REFERENCE: UF-230  
; CURRENT APPLICATION NUMBER: US/09/295,996B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TMOF peptide

US-09-295-996B-29

Query Match 38.3%; Score 31; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
:||||  
Db 4 YPPPP 8

Search completed: July 4, 2004, 04:48:50  
Job time : 10.403 secs



OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 11.5299 Seconds  
 (without alignments)  
 125.142 Million cell updates/sec

Title: US-09-641-802-7  
 Perfect score: 81  
 Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7  
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	31	38.3	17	2	S57991	hydroxyproline-ric
2	29	35.8	15	2	PT0037	light harvesting c
3	28	34.6	7	2	S71299	ICL2 protein - Par
4	28	34.6	10	2	A36454	trypsin-modulating
5	28	34.6	17	2	S59481	hydroxyproline-ric
6	27	33.3	12	2	B39690	neural cell adhesi
7	27	33.3	13	2	S21152	tryptophyllin-rela
8	27	33.3	16	2	JH0517	insulin-like growt
9	26	32.1	12	2	E45691	probable minor cap
10	26	32.1	13	2	D39690	neural cell adhesi
11	26	32.1	14	2	H64008	hypothetical prote
12	26	32.1	14	2	S12904	protein kinase (EC
13	26	32.1	16	2	E58503	superoxide dismuta

14	25	30.9	9	2	S26508	collagen alpha 2(V
15	25	30.9	12	2	PN0663	dystrophin-associa
16	24	29.6	11	2	C37196	bradykinin-potenti
17	24	29.6	11	2	D37196	bradykinin-potenti
18	24	29.6	11	2	D45900	complement C3b rec
19	24	29.6	13	2	B35245	histone H1.c - mou
20	24	29.6	13	2	A35245	histone H1a - mous
21	24	29.6	14	2	C33098	223K exoantigen -
22	24	29.6	17	2	A42920	fatty acid ethyl e
23	23	28.4	9	2	S66607	quinoline 2-oxidor
24	23	28.4	10	2	H28027	protein P11 - curl
25	23	28.4	13	2	A05174	tryptophyllin-13 -
26	23	28.4	15	2	A28965	ribulose-bisphosph
27	23	28.4	15	2	F28587	T-cell receptor be
28	23	28.4	15	2	I53284	T-cell receptor be
29	23	28.4	17	2	D53284	T-cell receptor be
30	23	28.4	18	2	A35704	cytochrome P450 ol
31	22.5	27.8	15	2	A54397	ubiquitin-carrier
32	22	27.2	8	2	S16324	hypothetical prote
33	22	27.2	13	2	PN0048	unidentified QM002
34	22	27.2	14	2	PA0104	protein QF200070 -
35	22	27.2	15	2	B39109	hypothetical 1.5K
36	22	27.2	15	2	PA0057	adenylate isopente
37	21	25.9	10	2	C35389	urease (EC 3.5.1.5
38	21	25.9	11	2	I52980	glucocerebrosidase
39	21	25.9	12	2	C39109	hypothetical 1.2K
40	21	25.9	12	2	PH1567	cerebrin 28 - huma
41	21	25.9	13	2	S09716	2S albumin large c
42	21	25.9	13	2	A40207	cell surface glyco
43	21	25.9	14	2	S11129	phosphoprotein, bo
44	21	25.9	15	2	B61457	alpha-glucosidase
45	21	25.9	18	2	PC2280	prolylendopeptidas
46	21	25.9	18	2	A54195	Na+/K+-exchanging
47	20	24.7	8	2	S21288	lectin - potato (f
48	20	24.7	10	2	B59272	peptide-N4- (N-acet
49	20	24.7	11	1	XASNBA	bradykinin-potenti
50	20	24.7	11	1	SPHO	substance P - hors
51	20	24.7	11	1	A60654	substance P - guin
52	20	24.7	11	2	S23306	substance P - Atla
53	20	24.7	12	2	S07436	tachykinin - Afric
54	20	24.7	12	2	PS0213	28K protein 4412 -
55	20	24.7	12	2	PA0098	ribosomal protein
56	20	24.7	13	2	G37266	Ig heavy chain C r
57	20	24.7	14	2	S48685	extension protein
58	20	24.7	14	2	PH0135	T-cell receptor be
59	20	24.7	14	2	S65392	cytochrome-c oxida
60	20	24.7	17	2	A49237	45/47K antigen - M
61	20	24.7	17	2	A39111	Ig light chain - P
62	20	24.7	17	2	B25348	glycogen(starch) s
63	19	23.5	10	2	S18396	probable glucose-6
64	19	23.5	10	2	C30572	T-cell receptor be
65	19	23.5	11	1	XAVIBH	bradykinin-potenti
66	19	23.5	11	2	JN0023	substance P - chic
67	19	23.5	11	2	D60409	kassinin-like pept
68	19	23.5	11	2	B60409	kassinin-like pept
69	19	23.5	11	2	C60409	kassinin-like pept
70	19	23.5	14	2	A42473	ermK leader peptid

71	19	23.5	14	2	C59137	protein Pf3 - gold
72	19	23.5	15	2	PA0002	photosystem II oxy
73	19	23.5	15	2	PA0014	seed storage prote
74	19	23.5	15	2	PN0173	seed storage prote
75	19	23.5	15	2	A41436	alpha-macroglobuli
76	19	23.5	15	2	PX0031	mixed lymphocyte r
77	19	23.5	15	2	B59137	protein Pf1 - gold
78	19	23.5	16	2	PH1302	Ig heavy chain DJ
79	19	23.5	16	2	JT0609	leukocyte chemoatt
80	19	23.5	16	2	PH0763	T-cell receptor be
81	19	23.5	16	2	PH0759	T-cell receptor be
82	19	23.5	16	2	A45454	ankyrin-binding gl
83	19	23.5	17	2	PT0235	Ig heavy chain CRD
84	19	23.5	18	2	A42576	steroid receptor c
85	18	22.2	8	2	A05169	neuropeptide M-I -
86	18	22.2	8	2	S10783	enamelin f - bovin
87	18	22.2	9	2	B30572	T-cell receptor be
88	18	22.2	10	1	XASNPC	angiotensin-conver
89	18	22.2	12	2	S11286	exo-alpha-sialidas
90	18	22.2	12	2	S67528	napin - rape (frag
91	18	22.2	12	2	JU0356	cycloleounurin -
92	18	22.2	13	2	A60856	inhibin alpha chai
93	18	22.2	13	2	S36668	hypothetical prote
94	18	22.2	13	2	S33800	chaperone, TCP1-re
95	18	22.2	14	2	A60737	pollen allergen Lo
96	18	22.2	14	2	S00150	ovostatin - duck (
97	18	22.2	14	2	E81280	probable proteolys
98	18	22.2	15	2	S29207	avenin gamma-4 - o
99	18	22.2	15	2	S67918	serine proteinase
100	18	22.2	15	2	A40634	orf19 3' of eryK -

#### ALIGNMENTS

##### RESULT 1

S57991

hydroxyproline-rich protein - Sesbania rostrata (fragment)

C;Species: Sesbania rostrata

C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 11-Jan-2000

C;Accession: S57991

R;Goormachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.;  
Holsters, M.; de Bruijn, F.

submitted to the EMBL Data Library, March 1995

A;Description: Use of differential display to identify novel Sesbania rostrata  
genes enhanced by Azorhizobium caulinodans infection.

A;Reference number: S57991

A;Accession: S57991

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-17 <GOO>

A;Cross-references: EMBL:Z48673; NID:g899484; PID:g899485

C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 38.3%; Score 31; DB 2; Length 17;

Best Local Similarity 83.3%; Pred. No. 88;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPP 10  
 | |||  
Db 8 KSPPPP 13

RESULT 2

PT0037

light harvesting complex chain III/b, photosystem I - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993

C;Accession: PT0037; PS0205

R;Uchiyama, Y.; Tsugita, A.

submitted to JIPID, June 1991

A;Reference number: PS0189

A;Accession: PT0037

A;Molecule type: protein

A;Residues: 1-15 <UCH>

Query Match 35.8%; Score 29; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPP 10  
 | |||  
Db 4 EAAAPPPP 11

RESULT 3

S71299

ICL2 protein - Paramecium tetraurelia (fragment)

C;Species: Paramecium tetraurelia

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

C;Accession: S71299

R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A;Title: Characterization of centrin genes in Paramecium.

A;Reference number: S71298; MUID:96248429; PMID:8665928

A;Accession: S71299

A;Molecule type: protein

A;Residues: 1-7 <MAD>

A;Experimental source: strain d4-2

C;Genetics:

A;Genetic code: SGC5

Query Match 34.6%; Score 28; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPQE 12  
 ||||:  
Db 3 PPPQQ 7

RESULT 4

A36454

trypsin-modulating oostatic factor - yellow fever mosquito

C;Species: *Aedes aegypti* (yellow fever mosquito)  
 C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 24-May-1996  
 C;Accession: A36454; A61630  
 R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
 FASEB J. 4, 3015-3020, 1990  
 A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme biosynthesis in the midgut.  
 A;Reference number: A36454; MUID:90367888; PMID:2394318  
 A;Accession: A36454  
 A;Molecule type: protein  
 A;Residues: 1-10 <BOR>  
 R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
 Insect Biochem. Mol. Biol. 23, 703-712, 1993  
 A;Title: Mass spectrometry and characterization of *Aedes aegypti* trypsin modulating oostatic factor (TMOF) and its analogs.  
 A;Reference number: A61630; MUID:93357794; PMID:8353526  
 A;Accession: A61630  
 A;Molecule type: protein  
 A;Residues: 1-10 <BO2>  
 A;Note: none of the amino acids is modified  
 C;Function:  
 A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut epithelial cells  
 C;Keywords: hormone

Query Match 34.6%; Score 28; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
 ||||  
 Db 5 PPPP 8

#### RESULT 5

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: *Phaseolus vulgaris* (kidney bean)

C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998

C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (*Phaseolus vulgaris* L.).

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 34.6%; Score 28; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10

Db                    ||||  
8 PPPP 11

RESULT 6

B39690

neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C;Accession: B39690  
R;Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA are expressed during rat heart development.  
A;Reference number: A39690; MUID:91141516; PMID:1996115  
A;Accession: B39690  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-12 <REY>  
A;Cross-references: GB:M63970  
C;Keywords: cardiac muscle; cell adhesion; heart

Query Match                    33.3%;   Score 27;   DB 2;   Length 12;  
Best Local Similarity       80.0%;   Pred. No. 2.4e+02;  
Matches       4;   Conservative       1;   Mismatches       0;   Indels       0;   Gaps       0;

Qy                    8 PPPQE 12  
                     |||:|  
Db                    6 PPPRE 10

RESULT 7

S21152

tryptophyllin-related peptide - two-colored leaf frog  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000  
C;Accession: S21152  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; Barra, D.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the Amazonian frog Phyllomedusa bicolor.  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21152  
A;Molecule type: protein  
A;Residues: 1-13 <MIG>  
A;Experimental source: skin  
C;Superfamily: unassigned animal peptides

Query Match                    33.3%;   Score 27;   DB 2;   Length 13;  
Best Local Similarity       62.5%;   Pred. No. 2.6e+02;  
Matches       5;   Conservative       0;   Mismatches       3;   Indels       0;   Gaps       0;

Qy                    3 EMKFPPPP 10  
                     | | |||  
Db                    2 EKPFYPPP 9

# RESULT 8

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 03-Nov-2003

C;Accession: JH0517

R;Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum.

A;Reference number: JH0515; MUID:92109718; PMID:1722398

A;Accession: JH0517

A;Molecule type: protein

A;Residues: 1-16 <COL>

A;Experimental source: serum

C;Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat homology

Query Match 33.3%; Score 27; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 3.3e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12

||| :|

Db 7 PPPSEE 12

# RESULT 9

E45691

probable minor capsid protein R117a [similarity] - *Lactobacillus delbrueckii* subsp. *lactis* phage LL-H (fragment)

C;Species: *Lactobacillus delbrueckii* subsp. *lactis* phage LL-H

C;Date: 24-Feb-1994 #sequence\_revision 25-Apr-1997 #text\_change 28-Jul-2000

C;Accession: E45691

R;Vasala, A.; Dupont, L.; Baumann, M.; Ritzenthaler, P.; Alatossava, T.

J. Virol. 67, 3061-3068, 1993

A;Title: Molecular comparison of the structural proteins encoding gene clusters of two related *Lactobacillus delbrueckii* bacteriophages.

A;Reference number: A45691; MUID:93267750; PMID:8497043

A;Accession: E45691

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <VAS>

A;Note: sequence extracted from NCBI backbone (NCBIN:132363, NCBIP:132373)

Query Match 32.1%; Score 26; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.4e+02;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 MKFPPPPQETVT 15

|| || | :

Db 1 MKLPIPYQMAVS 12

# RESULT 10

D39690

neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: D39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA are expressed during rat heart development.

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: D39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-13 <REY>

A;Cross-references: GB:M63970

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin homology

C;Keywords: cardiac muscle; cell adhesion; heart ,

Query Match 32.1%; Score 26; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPQ 11

||||

Db 6 PPPQ 9

RESULT 11

H64008

hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998

C;Accession: H64008

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;

Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.;

McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;

Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.;

Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen,

D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.;

Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.;

Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: H64008

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <TIGR>

A;Cross-references: GB:U32731; GB:L42023; NID:g1573465; PID:g1573478;

TIGR:HI0492

Query Match 32.1%; Score 26; DB 2; Length 14;

Best Local Similarity 57.1%; Pred. No. 4e+02;



Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 KFPPPPQ 11  
 | || |:  
 Db 7 KMPPKPK 13

RESULT 12

S12904

protein kinase (EC 2.7.1.37) - starfish (*Pisaster ochraceus*)

C;Species: *Pisaster ochraceus*

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997

C;Accession: S12904

R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
 FEBS Lett. 273, 223-226, 1990

A;Title: Identification of the sites in myelin basic protein that are phosphorylated by meiosis-activated protein kinase p44(mpk).

A;Reference number: S12904; MUID:91032186; PMID:1699809

A;Accession: S12904

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <SAN>

C;Keywords: phosphotransferase

Query Match 32.1%; Score 26; DB 2; Length 14;  
 Best Local Similarity 36.4%; Pred. No. 4e+02;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQ 11  
 :: : ||| |  
 Db 2 IVTPRTPPPSQ 12

RESULT 13

E58503

superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)

N;Alternate names: 21.3K bladder and kidney stone protein

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 05-Mar-1999

C;Accession: E58503

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: E58503

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <BIN>

A;Experimental source: human bladder and kidney stones

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen and hydrogen peroxide

C;Keywords: metalloprotein; oxidoreductase

Query Match 32.1%; Score 26; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQE 12  
:| |||  
Db 1 MEHTLPPLPYE 11

RESULT 14

S26508

collagen alpha 2(VI) chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Dec-1998

C;Accession: S26508

R;Jander, R.; Rautenberg, J.; Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and human short-chain collagen (intima collagen).

A;Reference number: S26506; MUID:83209648; PMID:6852033

A;Accession: S26508

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <JAN>

C;Keywords: hydroxyproline

F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.9%; Score 25; DB 2; Length 9;  
Best Local Similarity 55.6%; Pred. No. 2.8e+05;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPP 10  
||: |||  
Db 1 LEIPGPPGP 9

RESULT 15

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0663

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0663

A;Molecule type: protein

A;Residues: 1-12 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 30.9%; Score 25; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KFPPPPQE 12  
| |||  
Db 1 KAPLPPPE 8

# RESULT 16

C37196

bradykinin-potentiating peptide 3 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: C37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: C37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.6%; Score 24; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 6.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11

|| ||

Db 4 PPRPQ 8

# RESULT 17

D37196

bradykinin-potentiating peptide 4 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: D37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: D37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.6%; Score 24; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 6.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11

|| ||

Db 4 PPRPQ 8

# RESULT 18

D45900

complement C3b receptor type 2 - mouse (clone 12) (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: D45900

R;Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.

J. Immunol. 144, 3581-3591, 1990

A;Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1.

A;Reference number: A45900; MUID:90229754; PMID:2139460

A;Accession: D45900

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-11 <KUR>

Query Match 29.6%; Score 24; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPP 10

|: |||

Db 4 EISCDPPP 11

RESULT 19

B35245

histone H1.c - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997

C;Accession: B35245

R;Ajiro, K.; Shibata, K.; Nishikawa, Y.

J. Biol. Chem. 265, 6494-6500, 1990

A;Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differentiation of mouse neuroblastoma cells.

A;Reference number: A35245; MUID:90202935; PMID:1690730

A;Accession: B35245

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <AJI>

C;Superfamily: histone H1

C;Keywords: chromosomal protein; nucleosome

Query Match 29.6%; Score 24; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPPQETVT 15

|| | :|

Db 5 PPVSELIT 12

RESULT 20

A35245

histone H1a - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997  
C;Accession: A35245  
R;Ajiro, K.; Shibata, K.; Nishikawa, Y.  
J. Biol. Chem. 265, 6494-6500, 1990  
A;Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differentiation of mouse neuroblastoma cells.  
A;Reference number: A35245; MUID:90202935; PMID:1690730  
A;Accession: A35245  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <AJI>  
C;Superfamily: histone H1  
C;Keywords: chromosomal protein; nucleosome

Query Match 29.6%; Score 24; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPPQETVT 15  
|| | :|  
Db 5 PPVSELIT 12

#### RESULT 21

C33098

223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: C33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: C33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NIC>

Query Match 29.6%; Score 24; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPQE 12  
||||  
Db 3 PPQE 6

#### RESULT 22

A42920

fatty acid ethyl ester synthase-II - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

C;Accession: A42920

R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.

J. Biol. Chem. 267, 13217-13221, 1992

A;Title: Purification and characterization of fatty acid ethyl ester synthase-II from human myocardium.

A;Reference number: A42920; MUID:92317032; PMID:1618826

A;Accession: A42920  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-17 <BOR>  
A;Experimental source: myocardium  
A;Note: sequence extracted from NCBI backbone (NCBIP:107742)

Query Match 29.6%; Score 24; DB 2; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
||| |  
Db 3 PPDPDTT 9

#### RESULT 23

S66607

quinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S66607

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66607

A;Molecule type: protein

A;Residues: 1-9 <SCH>

A;Experimental source: strain 63

Query Match 28.4%; Score 23; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFP 7  
||||  
Db 1 MKFP 4

#### RESULT 24

H28027

protein P11 - curled-leaved tobacco (fragment)

C;Species: Nicotiana glauca (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993

C;Accession: H28027

R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-sequence analysis of proteins electroblotted from two-dimensional gel-separated total extracts.

A;Reference number: A94167

A;Accession: H28027

A;Molecule type: protein

A;Residues: 1-10 <BAU>

A;Note: 4-Val was also found

Query Match 28.4%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 7.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
: || ||  
Db 2 IKFEGPP 8

RESULT 25

A05174

tryptophyllin-13 - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 18-Aug-2000

C;Accession: A05174

R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.

Int. J. Pept. Protein Res. 27, 175-182, 1986

A;Reference number: A05174

A;Accession: A05174

A;Molecule type: protein

A;Residues: 1-13 <MON>

C;Superfamily: unassigned animal peptides

C;Keywords: pyroglutamic acid; skin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.4%; Score 23; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPP 10  
| : |||  
Db 2 EKPYPWPP 9

RESULT 26

A28965

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach  
(fragments)

C;Species: Spinacia oleracea (spinach)

C;Date: 22-Dec-1988 #sequence\_revision 22-Dec-1988 #text\_change 23-Feb-1997

C;Accession: A28965

R;Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988

A;Title: Reaction-intermediate analogue binding by ribulose bisphosphate  
carboxylase/oxygenase causes specific changes in proteolytic sensitivity: the  
amino-terminal residue of the large subunit is acetylated proline.

A;Reference number: A28965; MUID:88144466; PMID:3422748

A;Accession: A28965

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <MUL>

C;Keywords: carbon-carbon lyase; carboxy-lyase; chloroplast

Query Match 28.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 KFPPPPQETV 14  
|| | :||  
Db 6 KFEFPAMDTV 15

RESULT 27

F28587

T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999

C;Accession: F28587

R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985

A;Title: Organization and sequences of the diversity, joining, and constant region genes of the human T-cell receptor beta chain.

A;Reference number: A94081; MUID:86094276; PMID:3866244

A;Accession: F28587

A;Molecule type: DNA

A;Residues: 1-15 <TOY>

A;Cross-references: GB:M14159; NID:g338852; PIDN:AAA60681.1; PID:g553692

C;Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 46.2%; Pred. No. 1.2e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQETVT 15  
| | | : |||  
Db 3 EQYFGPGTRLTVT 15

RESULT 28

I53284

T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C;Accession: I53284

R;Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A;Title: Evolutionarily conserved organization and sequences of germline diversity and joining regions of the rabbit T-cell receptor beta 2 chain.

A;Reference number: A53284; MUID:91342695; PMID:1678859

A;Accession: I53284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-15 <HAR>

A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19525.1; PID:g233925

A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60747)

C;Keywords: T-cell receptor

Query Match 28.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 46.2%; Pred. No. 1.2e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQETVT 15



Db                   | | | : |||  
3 EQYFGPGTKLTVT 15

RESULT 29

D53284

T-cell receptor beta 2 chain J region, Jbeta2.1 - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C;Accession: D53284

R;Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A;Title: Evolutionarily conserved organization and sequences of germline diversity and joining regions of the rabbit T-cell receptor beta 2 chain.

A;Reference number: A53284; MUID:91342695; PMID:1678859

A;Accession: D53284

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-17 <HAR>

A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19520.1; PID:g233920

A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60742)

C;Keywords: T-cell receptor

Query Match                   28.4%; Score 23; DB 2; Length 17;  
Best Local Similarity       50.0%; Pred. No. 1.4e+03;  
Matches       6; Conservative       1; Mismatches       5; Indels       0; Gaps       0;

Qy                   3 EMKFPPPPQETV 14

| : | | | | |

Db                   5 ELFFGPGTQLTV 16

RESULT 30

A35704

cytochrome P450 olf2 - bovine (fragment)

N;Contains: oxidoreductase (EC 1.-.-.-)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 12-Mar-1999

C;Accession: A35704

R;Lazard, D.; Tal, N.; Rubinstein, M.; Khen, M.; Lancet, D.; Zupko, K.

Biochemistry 29, 7433-7440, 1990

A;Title: Identification and biochemical analysis of novel olfactory-specific cytochrome P-450IIA and UDP-glucuronosyl transferase.

A;Reference number: A35704; MUID:91027757; PMID:2121272

A;Accession: A35704

A;Molecule type: protein

A;Residues: 1-18 <LAZ>

C;Genetics:

A;Gene: CYP2A

C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protein

Query Match                   28.4%; Score 23; DB 2; Length 18;  
Best Local Similarity       44.4%; Pred. No. 1.5e+03;  
Matches       4; Conservative       2; Mismatches       3; Indels       0; Gaps       0;

Qy 4 MKFPPPPQE 12  
| : | ||:  
Db 1 MXYLPGPQQ 9

RESULT 31

A54397

ubiquitin-carrier protein E2-F1 - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Jan-2000

C;Accession: A54397

R;Blumenfeld, N.; Gonen, H.; Mayer, A.; Smith, C.E.; Siegel, N.R.; Schwartz, A.L.; Ciechanover, A.

J. Biol. Chem. 269, 9574-9581, 1994

A;Title: Purification and characterization of a novel species of ubiquitin-carrier protein, E2, that is involved in degradation of non-"N-end rule" protein substrates.

A;Reference number: A54397; MUID:94193635; PMID:8144544

A;Accession: A54397

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BLU>

A;Experimental source: reticulocyte

A;Note: sequence extracted from NCBI backbone (NCBIP:146038)

C;Superfamily: human ubiquitin-protein ligase E2

Query Match 27.8%; Score 22.5; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 1.5e+03;  
Matches 5; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

Qy 2 LEMKFP-----PP PQ 11  
:|: || ||:  
Db 1 IEINFPAEYPFKPPK 15

RESULT 32

S16324

hypothetical protein 2 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000

C;Accession: S16324

R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A;Title: A novel class of plant proteins containing a homeodomain with a closely linked leucine zipper motif.

A;Reference number: S16323; MUID:91266907; PMID:1675603

A;Accession: S16324

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-8 <RUB>

A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 27.2%; Score 22; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPP 9

Db                   :| | ||  
                    1 MEYKLLPP 8

RESULT 33

PN0048

unidentified QM0023 protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C;Accession: PN0048

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0048

A;Molecule type: protein

A;Residues: 1-13 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 30,500 and the pI is 6.19.

C;Keywords: brain

Query Match                   27.2%;   Score 22;   DB 2;   Length 13;  
Best Local Similarity   66.7%;   Pred. No. 1.5e+03;  
Matches       4;   Conservative       1;   Mismatches       1;   Indels       0;   Gaps       0;

Qy           10 PQETVT 15  
             | :|||  
Db           8 PXDTVT 13

RESULT 34

PA0104

protein QF200070 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0104

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichisides proteins.

A;Reference number: PA0051

A;Accession: PA0104

A;Molecule type: protein

A;Residues: 1-14 <CHO>

Query Match                   27.2%;   Score 22;   DB 2;   Length 14;  
Best Local Similarity   55.6%;   Pred. No. 1.6e+03;  
Matches       5;   Conservative       0;   Mismatches       4;   Indels       0;   Gaps       0;

Qy           3 EMKFPPPPQ 11  
             || | | |  
Db           3 EMXFAXPRQ 11

RESULT 35

B39109

hypothetical 1.5K protein - hepatitis C virus  
 N;Alternate names: hypothetical protein 2  
 C;Species: hepatitis C virus  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
 C;Accession: B39109; JQ1585  
 R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.;  
 Tekamp-Olson, P.; Kuo, G.; Choo, Q.L.; Houghton, M.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
 A;Title: Characterization of the terminal regions of hepatitis C viral RNA:  
 identification of conserved sequences in the 5' untranslated region and poly(A)  
 tails at the 3' end.  
 A;Reference number: A39109; MUID:91156678; PMID:1705704  
 A;Accession: B39109  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <HAN>  
 A;Cross-references: GB:M58406  
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
 J. Gen. Virol. 73, 1521-1525, 1992  
 A;Title: Cloning and sequencing of the structural region and expression of  
 putative core gene of hepatitis C virus from a British case of chronic sporadic  
 hepatitis.  
 A;Reference number: JQ1584; MUID:92300349; PMID:1318944  
 A;Accession: JQ1585  
 A;Molecule type: genomic RNA  
 A;Residues: 1-15 <KUM>  
 A;Experimental source: strain U.K.

Query Match 27.2%; Score 22; DB 2; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQE 12  
 |:: ||||  
 Db 3 VVQPPGPPLPGE 14

#### RESULT 36

PA0057

adenylate isopentenyltransferase (EC 2.5.1.27) - fungus (Fusarium  
 sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0057

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPIID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium  
 sporotrichisides proteins.

A;Reference number: PA0051

A;Accession: PA0057

A;Molecule type: protein

A;Residues: 1-15 <CHO>

C;Keywords: transferase

Query Match 27.2%; Score 22; DB 2; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQETV 14  
||:|:  
Db 4 PQQTI 8

RESULT 37

C35389

urease (EC 3.5.1.5) 6K chain - *Morganella morganii* (fragment)

C;Species: *Morganella morganii*

C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 23-Jun-1993

C;Accession: C35389

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A;Title: *Morganella morganii* urease: purification, characterization, and isolation of gene sequences.

A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: C35389

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HUA>

C;Keywords: hydrolase

Query Match 25.9%; Score 21; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
|: || |  
Db 1 MQLTPPEVE 9

RESULT 38

I52980

glucocerebrosidase - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I52980; I65971

R;Reiner, O.; Wigderson, M.; Horowitz, M.

DNA 7, 107-116, 1988

A;Title: Structural analysis of the human glucocerebrosidase genes.

A;Reference number: I52980; MUID:88195776; PMID:3359914

A;Accession: I52980

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024

A;Accession: I65971

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RE2>

A;Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

Query Match 25.9%; Score 21; DB 2; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1.8e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
|:| | :|  
Db 1 MEFSSPVRE 9

RESULT 39

C39109

hypothetical 1.2K protein - hepatitis C virus

N;Alternate names: hypothetical protein 3

C;Species: hepatitis C virus

C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999

C;Accession: C39109; JQ1586

R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-Olson, P.; Kuo, G.; Choo, Q.L.; Houghton, M.

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification of conserved sequences in the 5' untranslated region and poly(A) tails at the 3' end.

A;Reference number: A39109; MUJID:91156678; PMID:1705704

A;Accession: C39109

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-12 <HAN>

A;Cross-references: GB:M58406

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of putative core gene of hepatitis C virus from a British case of chronic sporadic hepatitis.

A;Reference number: JQ1584; MUJID:92300349; PMID:1318944

A;Accession: JQ1586

A;Molecule type: genomic RNA

A;Residues: 1-12 <KUM>

A;Experimental source: strain U.K.

Query Match 25.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPQE 12  
|||:  
Db 8. PPQD 11

RESULT 40

PH1567

cerebrin 28 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999

C;Accession: PH1567

R;Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y. J. Neurochem. 61, 533-540, 1993

A;Title: Micropurification of two human cerebrospinal fluid proteins by high performance electrophoresis chromatography.

A;Reference number: PH1566; MUJID:93329419; PMID:8336140

A;Accession: PH1567

A;Molecule type: protein

A;Residues: 1-12 <LEO>

Query Match 25.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 1.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PPPQETV 14  
|||:|  
Db 2 PPAQVSV 8

RESULT 41

S09716

2S albumin large chain (1 and 2) nII - rape (fragments)

N;Alternate names: 2S albumin large chain nIII

C;Species: Brassica napus (rape)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Aug-1998

C;Accession: S09716; S09718; S09717

R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.

FEBS Lett. 263, 209-212, 1990

A;Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins.

A;Reference number: S09720; MUID:90242974; PMID:2185951

A;Accession: S09716

A;Molecule type: protein

A;Residues: 1-9;10-13 <MON>

A;Experimental source: seed

A;Note: 3-Ser was also found

A;Accession: S09718

A;Molecule type: protein

A;Residues: 1-9;10-13 <MO2>

A;Experimental source: seed

A;Accession: S09717

A;Molecule type: protein

A;Residues: 1-9;10-13 <MO3>

A;Experimental source: seed

Query Match 25.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9  
|||  
Db 8 PPP 10

RESULT 42

A40207

cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum)  
(fragment)

C;Species: Dictyostelium discoideum

C;Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 31-Dec-1993

C;Accession: A40207

R;Gao, E.N.; Shier, P.; Siu, C.H.

J. Biol. Chem. 267, 9409-9415, 1992

A;Title: Purification and partial characterization of a cell adhesion molecule (gp150) involved in postaggregation stage cell-cell binding in Dictyostelium discoideum.

A;Reference number: A40207; MUID:92250549; PMID:1577768

A;Accession: A40207

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <GAO>

C;Keywords: glycoprotein

Query Match 25.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
|||:

Db 3 PPTPAD 8

#### RESULT 43

S11129

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 25-Oct-1996

C;Accession: S11129

R;Mikuni-Takagaki, Y.; Glimcher, M.J.

Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins.

Identification of the bone phosphoproteins of embryonic tibia.

A;Reference number: S11127; MUID:90303246; PMID:2363696

A;Accession: S11129

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MIK>

C;Keywords: phosphoprotein

Query Match 25.9%; Score 21; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9  
|||

Db 5 PPP 7

#### RESULT 44

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification and characterization.

A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457



A;Molecule type: protein  
A;Residues: 1-15 <BAN>  
C;Genetics:  
A;Genetic code: SGC5  
C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase;  
lysosome; monomer

Query Match 25.9%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPPQ 11  
| |||  
Db 5 FTPPLQ 10

RESULT 45

PC2280

prolylendopeptidase-inhibiting peptide - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997

C;Accession: PC2280

R;Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.

Biochem. Biophys. Res. Commun. 202, 809-815, 1994

A;Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.

A;Reference number: PC2280; MUID:94324971; PMID:8048952

A;Accession: PC2280

A;Molecule type: protein

A;Residues: 1-18 <OHM>

A;Experimental source: brain

C;Superfamily: cytoskeletal keratin

Query Match 25.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9  
|||  
Db 2 PPP 4

RESULT 46

A54195

Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 19-Apr-2002

C;Accession: A54195

R;Esmann, M.; Karlsh, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase from shark rectal glands.

A;Reference number: A54195; MUID:94297020; PMID:8025109

A;Accession: A54195

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <ESM>

A;Experimental source: rectal gland

A;Note: sequence extracted from NCBI backbone (NCBIP:149363)  
C;Keywords: hydrolase

Query Match 25.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9  
|||  
Db 8 PPP 10

RESULT 47

S21288

lectin - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998

C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding.

A;Reference number: S21288; MUID:92272683; PMID:1590771

A;Accession: S21288

A;Molecule type: protein

A;Residues: 1-8 <MIL>

A;Experimental source: var. Ulster Sceptre

C;Function:

A;Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 24.7%; Score 20; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPP 10  
| ||  
Db 5 PSPP 8

RESULT 48

B59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain - sweet almond (fragment)

N;Alternate names: peptide N-glycosidase

C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000

C;Accession: B59272

R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998

A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A and its N-glycans.

A;Reference number: A59272; MUID:98181894; PMID:9523720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>  
C;Keywords: hydrolase

Query Match 24.7%; Score 20; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPP 8  
|||  
Db 8 FPP 10

RESULT 49

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 24.7%; Score 20; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|||:  
Db 4 PPRPK 8

RESULT 50

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 24.7%; Score 20; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPPQE 12  
| ||:  
Db 2 PKPQQ 6

Search completed: July 4, 2004, 04:47:19  
Job time : 12.5299 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 29.4403 Seconds  
(without alignments)  
158.601 Million cell updates/sec

Title: US-09-641-802-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	81	100.0	15	14	US-10-281-652-7	Sequence 7, Appli
2	38	46.9	9	9	US-09-825-144-10	Sequence 10, Appl
3	37	45.7	18	9	US-09-879-957-165	Sequence 165, App
4	37	45.7	18	14	US-10-185-050-109	Sequence 109, App
5	37	45.7	18	14	US-10-161-791-305	Sequence 305, App
6	36	44.4	14	9	US-09-825-144-12	Sequence 12, Appl
7	36	44.4	15	9	US-09-825-144-1	Sequence 1, Appli
8	35	43.2	10	9	US-09-823-240-1	Sequence 1, Appli
9	35	43.2	10	11	US-09-261-894-19	Sequence 19, Appl
10	35	43.2	12	11	US-09-261-894-161	Sequence 161, App
11	35	43.2	13	14	US-10-185-050-7	Sequence 7, Appli
12	35	43.2	15	14	US-10-161-791-349	Sequence 349, App
13	35	43.2	15	14	US-10-161-791-423	Sequence 423, App
14	35	43.2	16	11	US-09-261-894-1	Sequence 1, Appli
15	35	43.2	16	12	US-10-253-286-1	Sequence 1, Appli
16	35	43.2	16	14	US-10-197-000-1	Sequence 1, Appli
17	35	43.2	16	15	US-10-245-871-1	Sequence 1, Appli
18	35	43.2	17	14	US-10-225-567A-2084	Sequence 2084, Ap
19	34	42.0	9	9	US-09-823-240-7	Sequence 7, Appli
20	34	42.0	9	11	US-09-261-894-160	Sequence 160, App
21	34	42.0	10	11	US-09-261-894-18	Sequence 18, Appl
22	34	42.0	14	14	US-10-307-956-20	Sequence 20, Appl
23	34	42.0	15	14	US-10-185-050-55	Sequence 55, Appl
24	34	42.0	15	14	US-10-161-791-339	Sequence 339, App
25	34	42.0	15	14	US-10-161-791-405	Sequence 405, App
26	34	42.0	17	14	US-10-331-907-403	Sequence 403, App
27	33	40.7	7	14	US-10-281-652-14	Sequence 14, Appl
28	33	40.7	10	16	US-10-415-014-495	Sequence 495, App
29	33	40.7	10	16	US-10-415-014-554	Sequence 554, App
30	33	40.7	10	16	US-10-415-014-681	Sequence 681, App
31	33	40.7	11	15	US-10-437-708-135	Sequence 135, App
32	33	40.7	11	15	US-10-437-708-199	Sequence 199, App
33	33	40.7	12	9	US-09-879-957-144	Sequence 144, App
34	33	40.7	12	14	US-10-185-050-52	Sequence 52, Appl
35	33	40.7	12	14	US-10-185-050-88	Sequence 88, Appl
36	33	40.7	15	14	US-10-161-791-367	Sequence 367, App
37	33	40.7	15	14	US-10-161-791-373	Sequence 373, App
38	33	40.7	15	14	US-10-161-791-439	Sequence 439, App
39	33	40.7	16	14	US-10-185-050-11	Sequence 11, Appl
40	33	40.7	16	14	US-10-185-050-228	Sequence 228, App
41	33	40.7	17	14	US-10-161-791-336	Sequence 336, App
42	32	39.5	8	14	US-10-226-007-738	Sequence 738, App
43	32	39.5	8	14	US-10-226-007-751	Sequence 751, App
44	32	39.5	8	14	US-10-226-007-764	Sequence 764, App
45	32	39.5	8	14	US-10-226-007-1492	Sequence 1492, Ap
46	32	39.5	8	14	US-10-226-007-1493	Sequence 1493, Ap
47	32	39.5	8	14	US-10-022-066-378	Sequence 378, App
48	32	39.5	9	14	US-10-226-007-739	Sequence 739, App
49	32	39.5	9	14	US-10-226-007-752	Sequence 752, App
50	32	39.5	9	14	US-10-226-007-765	Sequence 765, App
51	32	39.5	9	14	US-10-226-007-778	Sequence 778, App
52	32	39.5	9	14	US-10-226-007-1025	Sequence 1025, Ap
53	32	39.5	9	14	US-10-226-007-1494	Sequence 1494, Ap
54	32	39.5	9	14	US-10-226-007-1496	Sequence 1496, Ap
55	32	39.5	10	14	US-10-226-007-740	Sequence 740, App
56	32	39.5	10	14	US-10-226-007-753	Sequence 753, App

57	32	39.5	10	14	US-10-226-007-766	Sequence 766, App
58	32	39.5	10	14	US-10-226-007-779	Sequence 779, App
59	32	39.5	10	14	US-10-226-007-791	Sequence 791, App
60	32	39.5	10	14	US-10-226-007-1026	Sequence 1026, Ap
61	32	39.5	10	14	US-10-226-007-1039	Sequence 1039, Ap
62	32	39.5	10	14	US-10-226-007-1497	Sequence 1497, Ap
63	32	39.5	10	14	US-10-226-007-1499	Sequence 1499, Ap
64	32	39.5	11	14	US-10-226-007-741	Sequence 741, App
65	32	39.5	11	14	US-10-226-007-754	Sequence 754, App
66	32	39.5	11	14	US-10-226-007-767	Sequence 767, App
67	32	39.5	11	14	US-10-226-007-780	Sequence 780, App
68	32	39.5	11	14	US-10-226-007-792	Sequence 792, App
69	32	39.5	11	14	US-10-226-007-803	Sequence 803, App
70	32	39.5	11	14	US-10-226-007-1027	Sequence 1027, Ap
71	32	39.5	11	14	US-10-226-007-1040	Sequence 1040, Ap
72	32	39.5	11	14	US-10-226-007-1053	Sequence 1053, Ap
73	32	39.5	11	14	US-10-226-007-1500	Sequence 1500, Ap
74	32	39.5	11	14	US-10-226-007-1502	Sequence 1502, Ap
75	32	39.5	12	10	US-09-990-832C-96	Sequence 96, Appl
76	32	39.5	12	14	US-10-226-007-742	Sequence 742, App
77	32	39.5	12	14	US-10-226-007-755	Sequence 755, App
78	32	39.5	12	14	US-10-226-007-768	Sequence 768, App
79	32	39.5	12	14	US-10-226-007-781	Sequence 781, App
80	32	39.5	12	14	US-10-226-007-793	Sequence 793, App
81	32	39.5	12	14	US-10-226-007-804	Sequence 804, App
82	32	39.5	12	14	US-10-226-007-814	Sequence 814, App
83	32	39.5	12	14	US-10-226-007-1028	Sequence 1028, Ap
84	32	39.5	12	14	US-10-226-007-1041	Sequence 1041, Ap
85	32	39.5	12	14	US-10-226-007-1054	Sequence 1054, Ap
86	32	39.5	12	14	US-10-226-007-1067	Sequence 1067, Ap
87	32	39.5	12	14	US-10-226-007-1503	Sequence 1503, Ap
88	32	39.5	12	14	US-10-226-007-1505	Sequence 1505, Ap
89	32	39.5	13	14	US-10-226-007-743	Sequence 743, App
90	32	39.5	13	14	US-10-226-007-756	Sequence 756, App
91	32	39.5	13	14	US-10-226-007-769	Sequence 769, App
92	32	39.5	13	14	US-10-226-007-782	Sequence 782, App
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94	32	39.5	13	14	US-10-226-007-805	Sequence 805, App
95	32	39.5	13	14	US-10-226-007-815	Sequence 815, App
96	32	39.5	13	14	US-10-226-007-824	Sequence 824, App
97	32	39.5	13	14	US-10-226-007-1029	Sequence 1029, Ap
98	32	39.5	13	14	US-10-226-007-1042	Sequence 1042, Ap
99	32	39.5	13	14	US-10-226-007-1055	Sequence 1055, Ap
100	32	39.5	13	14	US-10-226-007-1068	Sequence 1068, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-281-652-7

; Sequence 7, Application US/10281652

; Publication No. US20030091606A1

##### ; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

```
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-7
```

```
Query Match          100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VLEMKFPPPPQETVT 15
          |||||
Db      1 VLEMKFPPPPQETVT 15
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#### RESULT 2

```
US-09-825-144-10
; Sequence 10, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-10
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```
Query Match          46.9%; Score 38; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.2e+06;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      6 FPPPPQETV 14
```



Db               ||||| : :  
                  1 FPPPPDDDI 9

RESULT 3

US-09-879-957-165

; Sequence 165, Application US/09879957

; Patent No. US20020034755A1

;   GENERAL INFORMATION:

;       APPLICANT: SPARKS, Andrew B.

;               HOFFMAN, No. US20020034755A1h

;               KAY, Brian K.

;               FOWLKES, Dana M.

;               McCONNELL, Stephen J.

;   TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

;               DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

;               USING SAME

;   NUMBER OF SEQUENCES: 227

;   CORRESPONDENCE ADDRESS:

;       ADDRESSEE: Pennie & Edmonds LLP

;       STREET: 1155 Avenue of the Americas

;       CITY: New York

;       STATE: New York

;       COUNTRY: USA

;       ZIP: 10036-2711

;   COMPUTER READABLE FORM:

;       MEDIUM TYPE: Floppy disk

;       COMPUTER: IBM PC compatible

;       OPERATING SYSTEM: PC-DOS/MS-DOS

;       SOFTWARE: PatentIn Release #1.0, Version #1.30

;   CURRENT APPLICATION DATA:

;       APPLICATION NUMBER: US/09/879,957

;       FILING DATE: 13-Jun-2001

;       CLASSIFICATION: <Unknown>

;   PRIOR APPLICATION DATA:

;       APPLICATION NUMBER: US 08/630,915

;       FILING DATE: 03-APR-1996

;   ATTORNEY/AGENT INFORMATION:

;       NAME: Misrock, S. Leslie

;       REGISTRATION NUMBER: 18,872

;       REFERENCE/DOCKET NUMBER: 1101-174

;   TELECOMMUNICATION INFORMATION:

;       TELEPHONE: (212) 790-9090

;       TELEFAX: (212) 869-8864/9741

;       TELEX: 66141 PENNIE

;   INFORMATION FOR SEQ ID NO: 165:

;       SEQUENCE CHARACTERISTICS:

;               LENGTH: 18 amino acids

;               TYPE: amino acid

;               STRANDEDNESS: <Unknown>

;               TOPOLOGY: unknown

;       MOLECULE TYPE: peptide

;       SEQUENCE DESCRIPTION: SEQ ID NO: 165:

US-09-879-957-165

Query Match               45.7%;   Score 37;   DB 9;   Length 18;  
Best Local Similarity   60.0%;   Pred. No. 2e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
 | |||| :  
 Db 7 EPDFPPPPPD 16

RESULT 4

US-10-185-050-109

; Sequence 109, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516

; FILING DATE: 03-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-208-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 109:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 109:

US-10-185-050-109

Query Match 45.7%; Score 37; DB 14; Length 18;

Best Local Similarity 60.0%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQE 12  
| |||| :  
Db 7 EPDFPPPPPD 16

RESULT 5

US-10-161-791-305

; Sequence 305, Application US/10161791

; Publication No. US20030186863A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 305:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-10-161-791-305

Query Match 45.7%; Score 37; DB 14; Length 18;  
Best Local Similarity 55.6%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FPPPPQETV 14  
||||| : :  
Db 7 FPPPPYQPI 15

RESULT 6

US-09-825-144-12

; Sequence 12, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-825-144-12

Query Match 44.4%; Score 36; DB 9; Length 14;  
Best Local Similarity 62.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPPQE 12  
:||||| :  
Db 2 EFPPPPPTD 9

RESULT 7

US-09-825-144-1

; Sequence 1, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-825-144-1

Query Match 44.4%; Score 36; DB 9; Length 15;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPPQE 12  
:||||| :  
Db 3 EFPPPPPTD 10

RESULT 8

US-09-823-240-1  
; Sequence 1, Application US/09823240  
; Patent No. US20020048813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jurgen Wehland  
; APPLICANT: Joseph Loureio  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa is Asp or Glu  
; NAME/KEY: UNSURE  
; LOCATION: (7)...(7)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-823-240-1

Query Match 43.2%; Score 35; DB 9; Length 10;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPPPPQE 12  
||||| :  
Db 2 FPPPPXD 8

RESULT 9

US-09-261-894-19

```
; Sequence 19, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
;   APPLICANT:  Humphreys, Robert E
;   APPLICANT:  Adams, Sharlene
;   APPLICANT:  Xu, Minzhen
;   TITLE OF INVENTION:  IMMUNOTHERAPY BY MODULATION OF ANTIGEN
;   NUMBER OF SEQUENCES:  165
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Kevin M. Farrell, P.C.
;     STREET:    P.O. Box 999
;     CITY:      York Harbor
;     STATE:     ME
;     COUNTRY:   USA
;     ZIP:       03911
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/261,894
;     FILING DATE:       March 3, 1999
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Farrell, Kevin M
;     REGISTRATION NUMBER:  35,505
;     REFERENCE/DOCKET NUMBER:  REH-9601
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (207) 363-0558
;     TELEFAX:   (207) 363-0528
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-261-894-19
```

```
Query Match          43.2%;  Score 35;  DB 11;  Length 10;
Best Local Similarity 60.0%;  Pred. No. 2.1e+02;
Matches      6;  Conservative    1;  Mismatches    3;  Indels      0;  Gaps      0;
```

```
Qy      2 LEMKFPPPPQ 11
        | | | | |
Db      1 LRMKLPKPPK 10
```

RESULT 10

US-09-261-894-161

```
; Sequence 161, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
;   APPLICANT:  Humphreys, Robert E
```

```

; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-161

```

```

Query Match          43.2%; Score 35; DB 11; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches      6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 LEMKFPPPPQ 11
        | || | ||:
Db      1 LRMKLPKPPK 10

```

```

RESULT 11
US-10-185-050-7
; Sequence 7, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
;           Kay, Brian K.
;           Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
;                   POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME
; NUMBER OF SEQUENCES: 233

```

```

;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: PENNIE & EDMONDS LLP
;      STREET: 1155 Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: USA
;      ZIP: 10036-2711
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/185,050
;      FILING DATE: 28-Jun-2002
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/826,516
;      FILING DATE: 03-Apr-1997
;      ATTORNEY/AGENT INFORMATION:
;      NAME: MISROCK, S. LESLIE
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 1101-208-999
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 896-8864/9741
;      TELEX: 66141 PENNIE
;      INFORMATION FOR SEQ ID NO: 7:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 13 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: <Unknown>
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-185-050-7

```

```

Query Match          43.2%; Score 35; DB 14; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches      5; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      6 FPPPPQE 12
        :|||| |
Db      5 YPPPPPE 11

```

```

RESULT 12
US-10-161-791-349
; Sequence 349, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

```



```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-349

```

```

Query Match          43.2%; Score 35; DB 14; Length 15;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches      6; Conservative      2; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      2 LEMKFPPPPQE 12
        | : ||||:
Db      1 LPSREPPPPQK 11

```

# RESULT 13

```

US-10-161-791-423
; Sequence 423, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.

```

```

; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-423

```

```

Query Match          43.2%; Score 35; DB 14; Length 15;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches      5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 PPPPQE 12
        ||||:|
Db      8 PPPPEE 13

```

```

RESULT 14
US-09-261-894-1
; Sequence 1, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene

```

```

; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-1

```

```

Query Match          43.2%; Score 35; DB 11; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches      6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 LEMKFPPPPQ 11
        | || | ||:
Db      1 LRMKLPKPPK 10

```

# RESULT 15

US-10-253-286-1

```

; Sequence 1, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17

```

; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Mammalian Ii-key  
; OTHER INFORMATION: peptide  
US-10-253-286-1

Query Match 43.2%; Score 35; DB 12; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11  
| || | ||:  
Db 1 LRMKLPKPPK 10

RESULT 16

US-10-197-000-1

; Sequence 1, Application US/10197000  
; Publication No. US20030091582A1  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E.  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE  
; FILE REFERENCE: REH2007  
; CURRENT APPLICATION NUMBER: US/10/197,000  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Mouse  
US-10-197-000-1

Query Match 43.2%; Score 35; DB 14; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPPPQ 11  
| || | ||:  
Db 1 LRMKLPKPPK 10

RESULT 17

US-10-245-871-1

; Sequence 1, Application US/10245871  
; Publication No. US20030235594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT

```
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian Ii-key
; OTHER INFORMATION: peptide
US-10-245-871-1
```

```
Query Match          43.2%; Score 35; DB 15; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches      6; Conservative      1; Mismatches      3; Indels      0; Gaps      0;
```

```
Qy      2 LEMKFPPPPQ 11
        | || | ||:
Db      1 LRMKLPKPPK 10
```

#### RESULT 18

```
US-10-225-567A-2084
; Sequence 2084, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2084
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2084
```

```
Query Match          43.2%; Score 35; DB 14; Length 17;
Best Local Similarity 70.0%; Pred. No. 3.5e+02;
Matches      7; Conservative      0; Mismatches      3; Indels      0; Gaps      0;
```

Qy 2 LEMKFPPPPQ 11  
|| | || ||  
Db 2 LEAKAPPRPQ 11

RESULT 19

US-09-823-240-7

; Sequence 7, Application US/09823240  
; Patent No. US20020048813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear  
; APPLICANT: Jurgen Wehland  
; APPLICANT: Joseph Loureio  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (9)...(9)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-823-240-7

Query Match 42.0%; Score 34; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
|||||  
Db 1 FPPPP 5

RESULT 20

US-09-261-894-160

; Sequence 160, Application US/09261894  
; Publication No. US20030207324A1  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E  
; APPLICANT: Adams, Sharlene  
; APPLICANT: Xu, Minzhen  
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: ME

```

; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-160

```

```

Query Match          42.0%; Score 34; DB 11; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches      6; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      2 LEMKFPPPP 10
        | || | ||
Db      1 LRMKLPKPP 9

```

# RESULT 21

US-09-261-894-18

```

; Sequence 18, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-18

```

```

Query Match          42.0%; Score 34; DB 11; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches      6; Conservative    0; Mismatches    3; Indels      0; Gaps      0;

```

```

Qy      2 LEMKFPPPP 10
        | | | | |
Db      1 LRMKLPKPP 9

```

# RESULT 22

```

US-10-307-956-20
; Sequence 20, Application US/10307956
; Publication No. US20030119072A1
; GENERAL INFORMATION:
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Xie, Weilin
; APPLICANT: Murray, Brion
; APPLICANT: Mercurio, Frank
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
; TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
; FILE REFERENCE: 860098.433
; CURRENT APPLICATION NUMBER: US/10/307,956
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/385,918
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-307-956-20

```

```

Query Match          42.0%; Score 34; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches      5; Conservative    2; Mismatches    1; Indels      0; Gaps      0;

```



Qy 3 EMKFPPPP 10  
|:: |||  
Db 1 ELESPPPP 8

RESULT 23

US-10-185-050-55

; Sequence 55, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516

; FILING DATE: 03-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-208-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 55:

US-10-185-050-55

Query Match 42.0%; Score 34; DB 14; Length 15;  
Best Local Similarity 75.0%; Pred. No. 4.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQETV 14  
|||| ||

Db 4 PPPPPYTV 11

RESULT 24

US-10-161-791-339

; Sequence 339, Application US/10161791

; Publication No. US20030186863A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 339:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-10-161-791-339

Query Match 42.0%; Score 34; DB 14; Length 15;  
Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
||||:  
Db 6 PPPPQK 11

RESULT 25

US-10-161-791-405

; Sequence 405, Application US/10161791

; Publication No. US20030186863A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 405:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-10-161-791-405

Query Match 42.0%; Score 34; DB 14; Length 15;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPPQ 11  
| | | | |  
Db 4 KPPPPQ 10

RESULT 26

US-10-331-907-403

; Sequence 403, Application US/10331907

; Publication No. US20030181660A1

; GENERAL INFORMATION:

; APPLICANT: Todd, John A  
; Hess, John W  
; Caskey, Charles T  
; Cox, Roger D  
; Gerhold, David  
; Hammond, Holly  
; Hey, Patricia  
; Kawaguchi, Yoshihiko  
; Merriman, Tony R  
; Metzker, Michael L

; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor

; NUMBER OF SEQUENCES: 455

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon and Vanderhye  
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: VA 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/331,907  
; FILING DATE: 31-Dec-2002

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/402,923A  
; FILING DATE: 14-Feb-2001  
; APPLICATION NUMBER: PCT/GB98/01102  
; FILING DATE: 15-APR-1998  
; APPLICATION NUMBER: US 60/043,553  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 60/048,740  
; FILING DATE: 05-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: B.J.Sadoff  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 620-81

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4091  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 403:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:  
US-10-331-907-403

Query Match 42.0%; Score 34; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10  
|||||  
Db 6 FPPPP 10

RESULT 27

US-10-281-652-14

; Sequence 14, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-14

Query Match 40.7%; Score 33; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|||||  
Db 2 PPPPQ 6

RESULT 28

US-10-415-014-495  
; Sequence 495, Application US/10415014  
; Publication No. US20040110674A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF  
CANCER  
; FILE REFERENCE: 511582004300  
; CURRENT APPLICATION NUMBER: US/10/415,014  
; CURRENT FILING DATE: 2003-11-19  
; PRIOR APPLICATION NUMBER: PCT/US02/27760  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/316,664  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 495  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-415-014-495

Query Match 40.7%; Score 33; DB 16; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
| |||| |  
Db 1 MNRPPPPVE 9

# RESULT 29

US-10-415-014-554  
; Sequence 554, Application US/10415014  
; Publication No. US20040110674A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF  
CANCER  
; FILE REFERENCE: 511582004300  
; CURRENT APPLICATION NUMBER: US/10/415,014  
; CURRENT FILING DATE: 2003-11-19  
; PRIOR APPLICATION NUMBER: PCT/US02/27760  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/316,664  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 736

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 554  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-415-014-554

Query Match 40.7%; Score 33; DB 16; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
| |||||  
Db 1 MNRPPPPVE 9

RESULT 30

US-10-415-014-681  
; Sequence 681, Application US/10415014  
; Publication No. US20040110674A1  
; GENERAL INFORMATION:  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
; TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF  
CANCER  
; FILE REFERENCE: 511582004300  
; CURRENT APPLICATION NUMBER: US/10/415,014  
; CURRENT FILING DATE: 2003-11-19  
; PRIOR APPLICATION NUMBER: PCT/US02/27760  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 60/316,664  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 736  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 681  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-415-014-681

Query Match 40.7%; Score 33; DB 16; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
| |||||  
Db 1 MNRPPPPVE 9

RESULT 31

US-10-437-708-135  
; Sequence 135, Application US/10437708  
; Publication No. US20040009555A1

```

; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-
Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 135
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Acacia senegal
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-135

```

```

Query Match          40.7%; Score 33; DB 15; Length 11;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches      5; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      7 PPPPQET 13
        |||| |
Db      1 PPPPSST 7

```

# RESULT 32

```

US-10-437-708-199
; Sequence 199, Application US/10437708
; Publication No. US20040009555A1
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-
Rich
; TITLE OF INVENTION: Glycoproteins
; FILE REFERENCE: OHU-04089
; CURRENT APPLICATION NUMBER: US/10/437,708
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/09/547,693
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 199
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Acacia senegal
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(4)
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
US-10-437-708-199

```



Query Match 40.7%; Score 33; DB 15; Length 11;  
Best Local Similarity 71.4%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQET 13  
| | | | |  
Db 1 PPPPSST 7

RESULT 33

US-09-879-957-144

; Sequence 144, Application US/09879957

; Patent No. US20020034755A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; HOFFMAN, No. US20020034755A1h

; KAY, Brian K.

; FOWLKES, Dana M.

; McCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/879,957

; FILING DATE: 13-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,915

; FILING DATE: 03-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 144:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 144:  
US-09-879-957-144

Query Match 40.7%; Score 33; DB 9; Length 12;  
Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPPQ 11  
:||||:  
Db 5 YPPPE 10

RESULT 34

US-10-185-050-52

; Sequence 52, Application US/10185050  
; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-10-185-050-52

Query Match 40.7%; Score 33; DB 14; Length 12;  
Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPPQ 11  
:||||:  
Db 5 YPPPE 10

RESULT 35

US-10-185-050-88

; Sequence 88, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>

; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:  
US-10-185-050-88

Query Match 40.7%; Score 33; DB 14; Length 12;  
Best Local Similarity 66.7%; Pred. No. 4.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPPQ 11  
:||||:  
Db 5 YPPPE 10

RESULT 36

US-10-161-791-367

; Sequence 367, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 367:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-367

Query Match 40.7%; Score 33; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
| | | | |  
Db 9 PPPPQ 13

RESULT 37

US-10-161-791-373

; Sequence 373, Application US/10161791  
; Publication No. US20030186863A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 373:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-373

Query Match 40.7%; Score 33; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|||||  
Db 6 PPPPQ 10

RESULT 38

US-10-161-791-439

; Sequence 439, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 439:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-439

Query Match 40.7%; Score 33; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
| | | | |  
Db 6 PPPPQ 10

RESULT 39

US-10-185-050-11

; Sequence 11, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-185-050-11

Query Match 40.7%; Score 33; DB 14; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPPQ 11  
:||||:  
Db 9 YPPPE 14

RESULT 40

US-10-185-050-228

; Sequence 228, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516

; FILING DATE: 03-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-208-999

; TELECOMMUNICATION INFORMATION:



; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 896-8864/9741  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 228:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: <Unknown>  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 228:  
 US-10-185-050-228

Query Match 40.7%; Score 33; DB 14; Length 16;  
 Best Local Similarity 54.5%; Pred. No. 6.1e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MKFPPPPQETV 14  
 |: |||| |  
 Db 3 MRDPPPPYNYV 13

# RESULT 41

US-10-161-791-336

; Sequence 336, Application US/10161791  
 ; Publication No. US20030186863A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/161,791  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:

```

; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-336

```

```

Query Match          40.7%; Score 33; DB 14; Length 17;
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches      5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      5 KFPPPP 10
        | |||
Db      5 KMPPPP 10

```

RESULT 42

US-10-226-007-738

```

; Sequence 738, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-738

```

```

Query Match          39.5%; Score 32; DB 14; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches      5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      7 PPPPQE 12
        |||| |
Db      1 PPPPYE 6

```

RESULT 43

US-10-226-007-751

; Sequence 751, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 751  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-226-007-751

Query Match 39.5%; Score 32; DB 14; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
| | | | |  
Db 2 PPPPYE 7

RESULT 44

US-10-226-007-764

; Sequence 764, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 764  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4

US-10-226-007-764

Query Match 39.5%; Score 32; DB 14; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy            7 PPPPQE 12  
              | | | | |  
Db            3 PPPPYE 8

RESULT 45

US-10-226-007-1492

; Sequence 1492, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1492  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Lymphocytic choriomeningitis virus  
US-10-226-007-1492

Query Match                    39.5%; Score 32; DB 14; Length 8;  
Best Local Similarity    83.3%; Pred. No. 1.2e+06;  
Matches       5; Conservative    0; Mismatches    1; Indels       0; Gaps       0;

Qy            7 PPPPQE 12  
              | | | | |  
Db            2 PPPPYE 7

RESULT 46

US-10-226-007-1493

; Sequence 1493, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1493  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Lymphocytic choriomeningitis virus  
US-10-226-007-1493

Query Match 39.5%; Score 32; DB 14; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
|||||  
Db 3 PPPPYE 8

RESULT 47

US-10-022-066-378

; Sequence 378, Application US/10022066  
; Publication No. US20030166057A1  
; GENERAL INFORMATION:  
; APPLICANT: HILDEBRAND, WILLIAM H.  
; APPLICANT: PRILLIMAN, KILEY RAE  
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 6680.034  
; CURRENT APPLICATION NUMBER: US/10/022,066  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/256,410  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/256,409  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 09/465,321  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 09/974,366  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 378  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-022-066-378

Query Match 39.5%; Score 32; DB 14; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KFPPPP 10  
::||||  
Db 3 ZYPPPP 8

RESULT 48

US-10-226-007-739

; Sequence 739, Application US/10226007  
; Publication No. US20030105277A1

; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 739  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-226-007-739

Query Match 39.5%; Score 32; DB 14; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
    |||||  
Db 1 PPPPYE 6

RESULT 49

US-10-226-007-752  
; Sequence 752, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 752  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-226-007-752

Query Match 39.5%; Score 32; DB 14; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
    |||||

Db

2 PPPPYE 7

RESULT 50

US-10-226-007-765

; Sequence 765, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 765

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Human herpesvirus 4

US-10-226-007-765

Query Match 39.5%; Score 32; DB 14; Length 9;

Best Local Similarity 83.3%; Pred. No. 1.2e+06;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12

|||||

Db 3 PPPPYE 8

Search completed: July 4, 2004, 05:12:29

Job time : 29.4403 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 25.5224 Seconds  
(without alignments)  
185.436 Million cell updates/sec

Title: US-09-641-802-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description
-----							



1	33	40.7	16	6	Q9TQZ7	Q9tqz7 bos taurus
2	32	39.5	15	6	Q9TR14	Q9tr14 bos taurus
3	31	38.3	17	10	O49225	O49225 glycine max
4	31	38.3	17	10	Q41400	Q41400 sesbania ro
5	30	37.0	15	10	P82439	P82439 nicotiana t
6	28	34.6	17	6	Q9TR22	Q9tr22 bos taurus
7	26	32.1	12	4	Q9BZ49	Q9bz49 homo sapien
8	26	32.1	18	4	Q9UCT9	Q9uct9 homo sapien
9	25	30.9	17	13	Q9PRU7	Q9pru7 gallus gall
10	24	29.6	10	12	Q9Q0W9	Q9q0w9 polyomaviru
11	24	29.6	10	12	Q8JV70	Q8jv70 polyomaviru
12	24	29.6	10	12	Q9Q0W1	Q9q0w1 polyomaviru
13	24	29.6	10	12	Q8JV68	Q8jv68 polyomaviru
14	24	29.6	10	12	Q9Q0V9	Q9q0v9 polyomaviru
15	24	29.6	10	12	Q9Q0W7	Q9q0w7 polyomaviru
16	24	29.6	10	12	Q8JV66	Q8jv66 polyomaviru
17	24	29.6	10	12	Q9Q0V7	Q9q0v7 polyomaviru
18	24	29.6	10	12	Q8JV82	Q8jv82 polyomaviru
19	24	29.6	10	12	Q8JV76	Q8jv76 polyomaviru
20	24	29.6	10	12	Q8JV74	Q8jv74 polyomaviru
21	24	29.6	10	12	Q9Q0W5	Q9q0w5 polyomaviru
22	24	29.6	10	12	Q9Q0X3	Q9q0x3 polyomaviru
23	24	29.6	10	12	Q9Q0X5	Q9q0x5 polyomaviru
24	24	29.6	10	12	Q9Q0W3	Q9q0w3 polyomaviru
25	24	29.6	10	12	Q8JV80	Q8jv80 polyomaviru
26	24	29.6	10	12	Q9Q0X1	Q9q0x1 polyomaviru
27	24	29.6	10	12	Q9Q0X9	Q9q0x9 polyomaviru
28	24	29.6	10	12	Q8JV72	Q8jv72 polyomaviru
29	24	29.6	13	4	Q9UDC6	Q9udc6 homo sapien
30	24	29.6	15	4	Q9BXX4	Q9bxx4 homo sapien
31	24	29.6	17	4	Q9UDD6	Q9udd6 homo sapien
32	23	28.4	9	2	Q99193	Q99193 pseudomonas
33	23	28.4	17	2	Q9R4T1	Q9r4t1 rhodobacter
34	23	28.4	18	4	Q8NFB4	Q8nfb4 homo sapien
35	23	28.4	18	4	Q9H1I3	Q9h1i3 homo sapien
36	22	27.2	13	12	Q81781	Q81781 hepatitis c
37	22	27.2	15	6	Q9TRA6	Q9tra6 bos taurus
38	22	27.2	15	10	Q9S8N8	Q9s8n8 hordeum vul
39	22	27.2	15	10	Q9S929	Q9s929 glycine max
40	22	27.2	16	13	Q9PRU6	Q9pru6 gallus gall
41	22	27.2	17	11	Q9JLA7	Q9jla7 mus musculu
42	22	27.2	18	4	Q9UE42	Q9ue42 homo sapien
43	22	27.2	18	11	Q9JIE9	Q9jie9 mus musculu
44	22	27.2	18	12	Q84129	Q84129 influenzavi
45	21	25.9	11	4	Q9C057	Q9c057 homo sapien
46	21	25.9	11	10	P82436	P82436 nicotiana t
47	21	25.9	12	10	Q93X21	Q93x21 zea mays (m
48	21	25.9	15	6	Q9TR45	Q9tr45 bos taurus
49	21	25.9	16	14	Q7TM78	Q7tm78 uncultured
50	21	25.9	17	4	Q9UC43	Q9uc43 homo sapien
51	21	25.9	17	10	P83061	P83061 spinacia ol
52	21	25.9	18	4	Q9UCG7	Q9ucg7 homo sapien
53	21	25.9	18	4	Q14042	Q14042 homo sapien
54	21	25.9	18	8	Q8SKY0	Q8sky0 cuscutea ref
55	21	25.9	18	11	Q8R170	Q8r170 mus musculu
56	21	25.9	18	13	Q8QFT3	Q8qft3 gallus gall
57	20	24.7	10	10	P81898	P81898 prunus dulc

58	20	24.7	11	8	Q95EI4	Q95ei4 dendrochilu
59	20	24.7	12	5	O61574	O61574 ostertagia
60	20	24.7	12	8	Q95EJ8	Q95ej8 dendrochilu
61	20	24.7	12	8	Q95EI6	Q95ei6 dendrochilu
62	20	24.7	12	8	Q95EJ5	Q95ej5 dendrochilu
63	20	24.7	12	8	Q95EL0	Q95el0 dendrochilu
64	20	24.7	12	8	Q95EK0	Q95ek0 dendrochilu
65	20	24.7	12	8	Q95EL6	Q95el6 dendrochilu
66	20	24.7	12	8	Q95EM2	Q95em2 dendrochilu
67	20	24.7	12	8	Q95EK8	Q95ek8 dendrochilu
68	20	24.7	12	8	Q95EL2	Q95el2 dendrochilu
69	20	24.7	12	8	Q95EM0	Q95em0 dendrochilu
70	20	24.7	12	8	Q95EJ3	Q95ej3 dendrochilu
71	20	24.7	12	8	Q95EL8	Q95el8 dendrochilu
72	20	24.7	12	8	Q95EK6	Q95ek6 dendrochilu
73	20	24.7	12	8	Q95EK2	Q95ek2 dendrochilu
74	20	24.7	12	8	Q95EJ1	Q95ej1 dendrochilu
75	20	24.7	12	8	Q95EI2	Q95ei2 dendrochilu
76	20	24.7	12	8	Q95EI8	Q95ei8 dendrochilu
77	20	24.7	12	8	Q95EK4	Q95ek4 dendrochilu
78	20	24.7	12	10	P82441	P82441 nicotiana t
79	20	24.7	13	12	Q81769	Q81769 hepatitis c
80	20	24.7	13	12	Q81770	Q81770 hepatitis c
81	20	24.7	14	2	P81715	P81715 streptomyce
82	20	24.7	14	4	Q9P2A2	Q9p2a2 homo sapien
83	20	24.7	15	4	Q15344	Q15344 homo sapien
84	20	24.7	15	4	O00604	O00604 homo sapien
85	20	24.7	16	4	Q9UC52	Q9uc52 homo sapien
86	20	24.7	16	5	Q9TWN7	Q9twn7 toxoplasma
87	20	24.7	16	5	Q9TWK1	Q9twk1 mytilus edu
88	20	24.7	16	6	Q9BGG8	Q9bgg8 sorex arane
89	20	24.7	16	6	Q9TRD1	Q9trd1 sus scrofa
90	20	24.7	17	2	Q9R560	Q9r560 bacillus su
91	20	24.7	17	6	Q9TR78	Q9tr78 didelphis m
92	20	24.7	18	4	Q16167	Q16167 homo sapien
93	20	24.7	18	8	Q7YMC5	Q7ymc5 pogonatum s
94	20	24.7	18	10	Q9S8I7	Q9s8i7 oryza sativ
95	20	24.7	18	11	Q9QW62	Q9qw62 rattus sp.
96	19	23.5	9	4	Q9UCS8	Q9ucs8 homo sapien
97	19	23.5	9	5	Q9TWV0	Q9twv0 anthopleura
98	19	23.5	9	10	P82429	P82429 nicotiana t
99	19	23.5	9	10	P82440	P82440 nicotiana t
100	19	23.5	10	2	Q9R5T2	Q9r5t2 acetobacter

# ALIGNMENTS

## RESULT 1

Q9TQZ7

ID Q9TQZ7 PRELIMINARY; PRT; 16 AA.

AC Q9TQZ7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Factor H (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96202005; PubMed=8615824;  
 RA Soames C.J., Day A.J., Sim R.B.;  
 RT "Prediction from sequence comparisons of residues of factor H involved  
 RT in the interaction with complement component C3b.";  
 RL Biochem. J. 315:523-531(1996).  
 SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 40.7%; Score 33; DB 6; Length 16;  
 Best Local Similarity 54.5%; Pred. No. 88;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQET 13  
 : | ||| :||  
 Db 2 DCKEPPPRKET 12

## RESULT 2

Q9TR14

ID Q9TR14 PRELIMINARY; PRT; 15 AA.  
 AC Q9TR14;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide  
 DE (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96187584; PubMed=8611748;  
 RA Nakai Y., Nishimura T., Shimizu M., Arai S.;  
 RT "Effects of freezing on the proteolysis of beef during storage at 4  
 RT degrees C.";  
 RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).  
 SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79E4777 CRC64;

Query Match 39.5%; Score 32; DB 6; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPQ 12  
 |||||  
 Db 2 PPPAE 7

## RESULT 3

O49225

ID O49225 PRELIMINARY; PRT; 17 AA.

AC 049225;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hydroxyproline-rich glycoprotein (Fragment).  
 GN HRGP.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Essex; TISSUE=Root;  
 RX MEDLINE=94211912; PubMed=8159793;  
 RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;  
 RT "Isolation and characterization of three soybean extensin cDNAs."  
 RL Plant Physiol. 104:793-796(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Essex; TISSUE=Root;  
 RA Mahalingam R., Knap H.T.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF047052; AAC03558.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;  
  
 Query Match 38.3%; Score 31; DB 10; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 5 KFPPPP 10  
 | ||||  
 Db 9 KSPPPP 14

#### RESULT 4

Q41400

ID Q41400 PRELIMINARY; PRT; 17 AA.  
 AC Q41400;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hydroxyproline-rich protein (Fragment).  
 OS Sesbania rostrata.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.  
 OX NCBI\_TaxID=3895;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sesbania rostrata;  
 RC TISSUE=Bacterial infected stem located root primordia;  
 RX MEDLINE=96112737; PubMed=8664492;  
 RA Goormachtig S., Valerio-Lepiniec M., Szczyglowski K., Van Montagu M.,  
 RA Holsters M., De Bruijn F.;  
 RT "Use of differential display to identify novel Sesbania rostrata genes

RT enhanced by Azorhizobium caulinodans infection.";  
 RL Mol. Plant Microbe Interact. 8:816-824(1995).  
 DR EMBL; Z48673; CAA88592.1; -.  
 DR PIR; S57991; S57991.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 38.3%; Score 31; DB 10; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPPP 10  
 | ||||  
 Db 8 KSPPPP 13

# RESULT 5

P82439

ID P82439 PRELIMINARY; PRT; 15 AA.  
 AC P82439;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 200 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall; Hydroxylation.  
 FT MOD\_RES 6 6 HYDROXYLATION.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 37.0%; Score 30; DB 10; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
 ||||::  
 Db 7 PPPPKK 12

# RESULT 6

Q9TR22

ID Q9TR22 PRELIMINARY; PRT; 17 AA.

AC Q9TR22;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE NONAMELOGENIN glycoprotein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96126798; PubMed=8564801;  
 RA Punzi J.S., DenBesten P.K.;  
 RT "Purification of nonamelogenin proteins from bovine secretory  
 RT enamel.";  
 RL Calcif. Tissue Int. 57:379-384(1995).  
 SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match 34.6%; Score 28; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
 ||||  
 Db 8 PPPP 11

#### RESULT 7

Q9BZ49

ID Q9BZ49 PRELIMINARY; PRT; 12 AA.  
 AC Q9BZ49;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Glycophorin C (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,  
 RA Zimmerman P.A.;  
 RT "The association of the glycophorin C exon 3 deletion with  
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New  
 RT Guinea.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF342984; AAK01459.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 32.1%; Score 26; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPQ 11  
||||  
Db 9 PPPQ 12

RESULT 8

Q9UCT9

ID Q9UCT9 PRELIMINARY; PRT; 18 AA.  
AC Q9UCT9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE PRG=PROLINE-rich glycoprotein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91373355; PubMed=1894623;  
RA Gillece-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,  
RA Fisher S.J.;  
RT "Structure and bacterial receptor activity of a human salivary  
RT proline-rich glycoprotein.";  
RL J. Biol. Chem. 266:17358-17368(1991).  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.  
DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 32.1%; Score 26; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPQ 11  
||||  
Db 14 PPPQ 17

RESULT 9

Q9PRU7

ID Q9PRU7 PRELIMINARY; PRT; 17 AA.  
AC Q9PRU7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO  
DE (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=95105151; PubMed=7806494;  
 RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
 RA Yazaki Y., Hirai H.;  
 RT "Characterization, partial purification, and peptide sequencing of  
 RT p130, the main phosphoprotein associated with v-Crk oncoprotein."  
 RL J. Biol. Chem. 269:32740-32746(1994).  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1608 MW; 52EAB880A931F887 CRC64;

Query Match 30.9%; Score 25; DB 13; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
 || ||  
 Db 13 PPQPQ 17

# RESULT 10

Q9Q0W9

ID Q9Q0W9 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0W9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UMEA3;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119350; AAF24106.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

# RESULT 11

Q8JV70

ID Q8JV70 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV70;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)



DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 5;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304387; AAM97804.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

# RESULT 12

Q9QOW1

ID Q9QOW1 PRELIMINARY; PRT; 10 AA.  
 AC Q9QOW1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CSFB;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119354; AAF24114.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

RESULT 13

Q8JV68

ID Q8JV68 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV68;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 6;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304388; AAM97806.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | | | |  
 Db 5 KTPPP 9

RESULT 14

Q9Q0V9

ID Q9Q0V9 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0V9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CSFE;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119355; AAF24116.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| |||  
Db 5 KTPPP 9

RESULT 15

Q9QOW7

ID Q9QOW7 PRELIMINARY; PRT; 10 AA.  
AC Q9QOW7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NANCY2;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119351; AAF24108.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| |||  
Db 5 KTPPP 9

RESULT 16

Q8JV66

ID Q8JV66 PRELIMINARY; PRT; 10 AA.  
AC Q8JV66;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CSF K;  
RX MEDLINE=21465052; PubMed=11581397;

RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304389; AAM97808.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | | | |  
 Db 5 KTPPP 9

#### RESULT 17

Q9Q0V7

ID Q9Q0V7 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0V7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CSFJ;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage.";  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119356; AAF24118.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | | | |  
 Db 5 KTPPP 9

#### RESULT 18

Q8JV82

ID Q8JV82 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV82;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E1;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF303944; AAM97792.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| | | |  
Db 5 KTPPP 9

RESULT 19  
Q8JV76

ID Q8JV76 PRELIMINARY; PRT; 10 AA.  
AC Q8JV76;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USA2;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF303947; AAM97798.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| | | |  
Db 5 KTPPP 9

RESULT 20

Q8JV74

ID Q8JV74 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV74;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA3;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303948; AAM97800.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

RESULT 21

Q9Q0W5

ID Q9Q0W5 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0W5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PRETORIA3;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119352; AAF24110.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| |||  
Db 5 KTPPP 9

RESULT 22

Q9Q0X3

ID Q9Q0X3 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BCN8;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119348; AAF24102.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| |||  
Db 5 KTPPP 9

RESULT 23

Q9Q0X5

ID Q9Q0X5 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BCN16;  
RX MEDLINE=20087544; PubMed=10618230;

RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119347; AAF24100.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| |||  
Db 5 KTPPP 9

#### RESULT 24

Q9QOW3

ID Q9QOW3 PRELIMINARY; PRT; 10 AA.  
AC Q9QOW3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PRETORIAL;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119353; AAF24112.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| |||  
Db 5 KTPPP 9

#### RESULT 25

Q8JV80

ID Q8JV80 PRELIMINARY; PRT; 10 AA.  
AC Q8JV80;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).



OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E2;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303945; AAM97794.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

# RESULT 26

Q9Q0X1

ID Q9Q0X1 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0X1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCN15;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage.";  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119349; AAF24104.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

RESULT 27

Q9Q0X9

ID Q9Q0X9 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0X9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCNU;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119345; AAF24096.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
 | |||  
 Db 5 KTPPP 9

RESULT 28

Q8JV72

ID Q8JV72 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV72;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 4;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304386; AAM97802.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 29.6%; Score 24; DB 12; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
| | |  
Db 5 KTPPP 9

RESULT 29

Q9UDC6

ID Q9UDC6 PRELIMINARY; PRT; 13 AA.  
AC Q9UDC6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE ENDOTHELIUM-derived RELATING factor, nitric oxide synthase  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93054573; PubMed=1385404;  
RA Janssens S.P., Simouchi A., Quertermous T., Bloch D.B., Bloch K.D.;  
RT "Cloning and expression of a cDNA encoding human endothelium-derived  
RT relating factor/nitric oxide synthase."  
RL J. Biol. Chem. 267:22694-22694(1992).  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;

Query Match 29.6%; Score 24; DB 4; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FPPPPQET 13  
| | | : |  
Db 3 FDPPGSDT 10

RESULT 30

Q9BXX4

ID Q9BXX4 PRELIMINARY; PRT; 15 AA.  
AC Q9BXX4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Transcription factor PAX 5 (PAX5) (Fragment).  
GN PAX5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hirabayashi Y., Rahman M., Sasaki T.;

RT "Identification of a novel repressor element in the 5'UTR of human  
 RT BSAP/Pax5A.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21354098; PubMed=11460166;  
 RA Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,  
 RA Chaganti R.S.K., Kuppers R., Dalla-Favera R.;  
 RT "Hypermethylation of multiple proto-oncogenes in B-cell diffuse large-  
 RT cell lymphomas.";  
 RL Nature 412:341-346(2001).  
 DR EMBL; AF268279; AAK25737.1; -.  
 DR EMBL; AF386790; AAK70869.1; -.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match 29.6%; Score 24; DB 4; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMKFPPP 9  
 || :| |  
 Db 3 LEKNYPTP 10

# RESULT 31

## Q9UDD6

ID Q9UDD6 PRELIMINARY; PRT; 17 AA.  
 AC Q9UDD6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Fatty acid ETHYL ester synthase-II, FAEE synthase-II (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92317032; PubMed=1618826;  
 RA Bora P.S., Wu X., Spilburg C.A., Lange L.G.;  
 RT "Purification and characterization of fatty acid ethyl ester synthase-  
 RT II from human myocardium.";  
 RL J. Biol. Chem. 267:13217-13221(1992).  
 DR PIR; A42920; A42920.  
 DR GO; GO:0005829; C:cytosol; NAS.  
 DR GO; GO:0030339; F:fatty-acyl-ethyl-ester synthase activity; NAS.  
 DR GO; GO:0006067; P:ethanol metabolism; NAS.  
 DR GO; GO:0006631; P:fatty acid metabolism; NAS.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1755 MW; 3456973BF1B39273 CRC64;

Query Match 29.6%; Score 24; DB 4; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 3e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PPPQET 13  
|| | |  
Db 3 PPDPDTT 9

RESULT 32

Q99193

ID Q99193 PRELIMINARY; PRT; 9 AA.  
AC Q99193;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE RpoB beta-subunit of RNA polymerase (Fragment).  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M.,  
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;  
RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of  
RT RNA polymerase in Pseudomonas putida."  
RL Dokl. Biochem. 302:1261-1265(1988).  
DR EMBL; X15849; CAA33847.1; -.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 852 MW; 5B4167776DC76727 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKFPPPP 10  
| | ||  
Db 1 MLLPAPP 7

RESULT 33

Q9R4T1

ID Q9R4T1 PRELIMINARY; PRT; 17 AA.  
AC Q9R4T1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Periplasmic protein 5 (Fragment).  
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1063;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95160605; PubMed=7857198;  
RA Sabaty M., Gagnon J., Vermeglio A.;  
RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the  
RT photodenitrifier Rhodobacter sphaeroides forma sp. denitrificans under  
RT anaerobic or aerobic condition."  
RL Arch. Microbiol. 162:335-343(1994).

SQ SEQUENCE 17 AA; 1794 MW; 7E08852216815C71 CRC64;

Query Match 28.4%; Score 23; DB 2; Length 17;  
Best Local Similarity 33.3%; Pred. No. 4.4e+03;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 EMKFPPPPQETV 14  
|: :| | : |  
Db 1 EVAWPEKPSQLV 12

RESULT 34

Q8NFB4

ID Q8NFB4 PRELIMINARY; PRT; 18 AA.  
AC Q8NFB4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Mutant enamelins (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kida M., Ariga T.;  
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused  
RT by an enamelins gene mutation at exon-intron boundary.";  
RL J. Dent. Res. 0:0-0(2002).  
DR EMBL; AF530444; AAM97323.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3E8BE512 CRC64;

Query Match 28.4%; Score 23; DB 4; Length 18;  
Best Local Similarity 60.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPPP 9  
: |||  
Db 1 RLPPP 5

RESULT 35

Q9H1I3

ID Q9H1I3 PRELIMINARY; PRT; 18 AA.  
AC Q9H1I3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Retinoic acid receptor gamma (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Xu H., Clifford J.L.;  
 RT "Genomic organization of the human retinoic acid receptor gamma  
 RT gene.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY013704; AAG41595.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1964 MW; A284A1EFBB361A22 CRC64;

Query Match 28.4%; Score 23; DB 4; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 4.6e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LEMKFPPP 9  
 | : | : | |  
 Db 7 LKMEIPGP 14

# RESULT 36

Q81781  
 ID Q81781 PRELIMINARY; PRT; 13 AA.  
 AC Q81781;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Genome polyprotein (Fragment).  
 GN POLYPROTEIN.  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=111103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=T9;  
 RX MEDLINE=92279243; PubMed=1317578;  
 RA Bukh J., Purcell R.H., Miller R.H.;  
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
 CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 DR EMBL; M84846; AAA45698.1; -.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR002522; HCV\_capsid.  
 DR Pfam; PF01543; HCV\_capsid; 1.  
 KW Polyprotein.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1557 MW; 464CF7E1A42FC763 CRC64;

Query Match 27.2%; Score 22; DB 12; Length 13;  
 Best Local Similarity 37.5%; Pred. No. 4.9e+03;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQETV 14  
| | ::|:  
Db 5 PKPQRKTI 12

RESULT 37

Q9TRA6

ID Q9TRA6 PRELIMINARY; PRT; 15 AA.  
AC Q9TRA6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE PA700 subunit P31=ATP-dependent 20 S proteasome activator  
DE (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94342244; PubMed=8063704;  
RA DeMartino G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,  
RA Afendis S.J., Swaffield J.C., Slaughter C.A.;  
RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an  
RT ATPase containing multiple members of a nucleotide-binding protein  
RT family.";  
RL J. Biol. Chem. 269:20878-20884(1994).  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1659 MW; D189812E9389B755 CRC64;

Query Match 27.2%; Score 22; DB 6; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VLEMKFPP 8  
:|:| |  
Db 3 LLELNFLP 10

RESULT 38

Q9S8N8

ID Q9S8N8 PRELIMINARY; PRT; 15 AA.  
AC Q9S8N8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Protein E-22 (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94170739; PubMed=8125056;



RA Flengsrud R.;  
RT "Separation of acidic barley endosperm proteins by two-dimensional  
RT electrophoresis.";  
RL Electrophoresis 14:1060-1066(1993).  
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 27.2%; Score 22; DB 10; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPQET 13  
|||::  
Db 5 PPQQS 9

#### RESULT 39

Q9S929

ID Q9S929 PRELIMINARY; PRT; 15 AA.  
AC Q9S929;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Pyrroline-5-carboxylate reductase, P5CR (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91378472; PubMed=1898034;  
RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;  
RT "Pyrroline-5-carboxylate reductase in soybean nodules:  
RT isolation/partial primary structure/evidence for isozymes.";  
RL Arch. Biochem. Biophys. 288:350-357(1991).  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1715 MW; D9821F773F3DF524 CRC64;

Query Match 27.2%; Score 22; DB 10; Length 15;  
Best Local Similarity 41.7%; Pred. No. 5.7e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 MKFPPPPQETVT 15  
|: |||: |  
Db 1 MEIFPIPAESYT 12

#### RESULT 40

Q9PRU6

ID Q9PRU6 PRELIMINARY; PRT; 16 AA.  
AC Q9PRU6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO  
DE (Fragment).  
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95105151; PubMed=7806494;  
 RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
 RA Yazaki Y., Hirai H.;  
 RT "Characterization, partial purification, and peptide sequencing of  
 RT p130, the main phosphoprotein associated with v-Crk oncoprotein."  
 RL J. Biol. Chem. 269:32740-32746(1994).  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1480 MW; CAB880A931F8873F CRC64;

Query Match 27.2%; Score 22; DB 13; Length 16;  
 Best Local Similarity 71.4%; Pred. No. 6.1e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 7 PP--PPQ 11  
 || |||  
 Db 9 PPATPPQ 15

#### RESULT 41

Q9JLA7

ID Q9JLA7 PRELIMINARY; PRT; 17 AA.  
 AC Q9JLA7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Fibroblast growth factor homologous factor 3 isoform 1B  
 DE (Fragment).  
 GN FHF-3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20112823; PubMed=10644718;  
 RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;  
 RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors  
 RT Is Generated by Alternative Promoter Usage and Differential  
 RT Splicing."  
 RL J. Biol. Chem. 275:2589-2597(2000).  
 DR EMBL; AF199604; AAF31391.1; -.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1870 MW; 9A0E0364E696D949 CRC64;

Query Match 27.2%; Score 22; DB 11; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 6.4e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MKFPPPPQ 11  
 | | ||

Db 1 MSLSPEPQ 8

RESULT 42

Q9UE42

ID Q9UE42 PRELIMINARY; PRT; 18 AA.  
AC Q9UE42;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Collagen.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89325561; PubMed=2753125;  
RA Vikkula M., Peltonen L.;  
RT "Structural analyses of the polymorphic area in type II collagen  
RT gene.";  
RL FEBS Lett. 250:171-174(1989).  
DR EMBL; X16158; CAA34280.1; -.  
SQ SEQUENCE 18 AA; 1614 MW; 041D6170BD6D3FA5 CRC64;

Query Match 27.2%; Score 22; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 6.8e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 P P P P Q E 12  
| | | |  
Db 6 P G P P G E 11

RESULT 43

Q9JIE9

ID Q9JIE9 PRELIMINARY; PRT; 18 AA.  
AC Q9JIE9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Protein arginine N-methyltransferase 1 (Fragment).  
GN MRMT1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20307889; PubMed=10848611;  
RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;  
RT "Arginine N-methyltransferase 1 is required for early postimplantation  
RT mouse development, but cells deficient in the enzyme are viable.";  
RL Mol. Cell. Biol. 20:4859-4869(2000).  
DR EMBL; AF232718; AAF37294.1; -.  
DR GO; GO:0008168; F:methyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.

KW Methyltransferase; Transferase.

FT NON\_TER 1 1

FT NON\_TER 18 18

SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;

Query Match 27.2%; Score 22; DB 11; Length 18;

Best Local Similarity 44.4%; Pred. No. 6.8e+03;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12

| || :|

Db 10 MSLQPPLEE 18

#### RESULT 44

Q84129

ID Q84129 PRELIMINARY; PRT; 18 AA.

AC Q84129;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg  
8), COOH terminus of NS1 (Fragment).

OS Influenzavirus A.

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza A viruses.

OX NCBI\_TaxID=197911;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83303830; PubMed=6612993;

RA Parvin J.D., Young J.F., Palese P.;

RT "nonsense mutations affecting the lengths of the ns1 nonstructural  
proteins of influenza a virus isolates.";

RL Virology 128:512-517(1983).

DR EMBL; K00959; AAA43541.1; -.

DR GO; GO:0003723; F:RNA binding; IEA.

DR InterPro; IPR000256; Flu\_NS1.

DR Pfam; PF00600; Flu\_NS1; 1.

FT NON\_TER 1 1

SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;

Query Match 27.2%; Score 22; DB 12; Length 18;

Best Local Similarity 66.7%; Pred. No. 6.8e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPPQE 12

|| ||

Db 11 PPLPPE 16

#### RESULT 45

Q9C057

ID Q9C057 PRELIMINARY; PRT; 11 AA.

AC Q9C057;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE HEX (Fragment).  
 GN HEX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oyama Y., Kurabayashi M., Nagai R., Shimomura Y., Sekiguchi K.;  
 RT "Human Hex 5'-flanking sequence."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF182950; AAK12833.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1125 MW; 2644D7FE686761F7 CRC64;

Query Match 25.9%; Score 21; DB 4; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MKFPPP 9  
 |::||  
 Db 1 MQYPHP 6

RESULT 46  
 P82436

ID P82436 PRELIMINARY; PRT; 11 AA.  
 AC P82436;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 65 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture."  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

Query Match 25.9%; Score 21; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9

Db                    |||  
                      2 PPP 4

RESULT 47

Q93X21

ID    Q93X21            PRELIMINARY;            PRT;        12 AA.  
AC    Q93X21;  
DT    01-DEC-2001 (TrEMBLrel. 19, Created)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE    Polyubiquitin homolog (Fragment).  
OS    Zea mays (Maize).  
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC    PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX    NCBI\_TaxID=4577;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RC    STRAIN=cv. INRA 258; TISSUE=Leaf;  
RX    MEDLINE=96236829; PubMed=8680303;  
RA    Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;  
RT    "Heavy-metal-responsive genes in maize: identification and comparison  
RT    of their expression upon various forms of abiotic stress."  
RL    Planta 199:1-8(1996).  
DR    EMBL; S82313; AAB47175.1; -.  
FT    NON\_TER            1            1  
SQ    SEQUENCE    12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match                    25.9%; Score 21; DB 10; Length 12;  
Best Local Similarity    100.0%; Pred. No. 6.7e+03;  
Matches        3; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy                    7 PPP 9  
                      |||  
Db                    2 PPP 4

RESULT 48

Q9TR45

ID    Q9TR45            PRELIMINARY;            PRT;        15 AA.  
AC    Q9TR45;  
DT    01-MAY-2000 (TrEMBLrel. 13, Created)  
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT    01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE    Amphoterin homolog (Fragment).  
OS    Bos taurus (Bovine).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC    Bovidae; Bovinae; Bos.  
OX    NCBI\_TaxID=9913;  
RN    [1]  
RP    SEQUENCE.  
RX    MEDLINE=96029671; PubMed=7592757;  
RA    Hori O., Brett J., Slattey T., Cao R., Zhang J., Chen J.X.,  
RA    Nagashima M., Lundh E.R., Vijay S., Nitecki D.;  
RT    "The receptor for advanced glycation end products (RAGE) is a cellular

RT binding site for amphoterin. Mediation of neurite outgrowth and co-  
RT expression of rage and amphoterin in the developing nervous system.";  
RL J. Biol. Chem. 270:25752-25761(1995).  
SQ SEQUENCE 15 AA; 1757 MW; 390B9679501CE020 CRC64;

Query Match 25.9%; Score 21; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 8.3e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PPPQET 13  
|| ||  
Db 5 PPKGET 10

RESULT 49

Q7TM78

ID Q7TM78 PRELIMINARY; PRT; 16 AA.  
AC Q7TM78;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit  
DE (Fragment).  
GN RBCL.  
OS uncultured organism.  
OC unclassified; environmental samples.  
OX NCBI\_TaxID=155900;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=sample 2/01/4.8;  
RA Willerslev E., Hansen A.J., Binladen J., Brand T.B., Gilbert M.T.P.,  
RA Shairo B., Bunce M., Wiuf C., Gilichinsky D.A., Cooper A.;  
RT "Diverse plant and animal genetic records from holocene and  
RT pleistocene sediments.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY262604; AAP85185.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1452 MW; 25EB5989979F0406 CRC64;

Query Match 25.9%; Score 21; DB 14; Length 16;  
Best Local Similarity 75.0%; Pred. No. 8.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPQE 12  
||:|  
Db 4 PPEE 7

RESULT 50

Q9UC43

ID Q9UC43 PRELIMINARY; PRT; 17 AA.  
AC Q9UC43;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Interferon-alpha-induced protein (Fragment).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96132854; PubMed=8557639;  
RA Rich S.A., Bose M., Tempst P., Rudofsky U.H.;  
RT "Purification, microsequencing, and immunolocalization of p36, a new  
RT interferon-alpha-induced protein that is associated with human lupus  
RT inclusions.";  
RL J. Biol. Chem. 271:1118-1126(1996).  
SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match 25.9%; Score 21; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 9.4e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEMKFP 7  
:| |:|  
Db 12 VEQKYP 17

Search completed: July 4, 2004, 04:45:39  
Job time : 26.5224 secs



OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 5.14925 Seconds  
(without alignments)  
151.683 Million cell updates/sec

Title: US-09-641-802-7  
Perfect score: 81  
Sequence: 1 VLEMKFPPPPQETVT 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	33	40.7	15	1	PRP_MYCBO	P80149 mycobacteri
2	28	34.6	10	1	TMOF_AEDAE	P19425 aedes aegyp
3	27	33.3	16	1	IBP4_PIG	P24854 sus scrofa
4	24	29.6	11	1	BPP3_BOTIN	P30423 bothrops in
5	24	29.6	11	1	BPP4_BOTIN	P30424 bothrops in
6	23	28.4	10	1	Q2OB_COMTE	P80465 comamonas t
7	23	28.4	13	1	TY13_PHYRO	P04096 phyllomedus
8	23	28.4	18	1	CPAX_BOVIN	P22779 bos taurus
9	22	27.2	12	1	FIF1_SARBU	P83349 sarcophaga
10	22	27.2	12	1	HS9A_RAT	P82995 rattus norv
11	22	27.2	16	1	LEC_DELRE	P83511 delonix reg
12	22	27.2	17	1	APID_BOMPA	P81464 bombus pasc
13	21	25.9	10	1	URE3_MORMO	P17339 morganella
14	21	25.9	15	1	SODM_STRGR	P80733 streptomyce
15	20	24.7	7	1	UF04_MOUSE	P38642 mus musculu
16	20	24.7	11	1	BPPB_AGKHA	P01021 agkistrodon
17	20	24.7	11	1	TKNA_GADMO	P28498 gadus morhu

18	20	24.7	11	1	TKNA_HORSE	P01290	equus cabal
19	20	24.7	12	1	TKN2_KASMA	P08614	kassina mac
20	20	24.7	16	1	AF2S_MALPA	P83142	malva parvi
21	20	24.7	17	1	A45K_MYCBO	P80069	mycobacteri
22	19	23.5	10	1	UPA2_HUMAN	P30088	homo sapien
23	19	23.5	11	1	BPP_AGKHP	P04562	agkistrodon
24	19	23.5	11	1	TKN1_PSEGU	P42986	pseudophryn
25	19	23.5	11	1	TKN2_PSEGU	P42987	pseudophryn
26	19	23.5	11	1	TKN3_PSEGU	P42988	pseudophryn
27	19	23.5	11	1	TKNA_CHICK	P19850	gallus gall
28	19	23.5	14	1	LPER_BACLI	Q04303	bacillus li
29	19	23.5	14	1	MARI_ALTSP	P29399	alteromonas
30	19	23.5	15	1	MK1_PALPR	P80408	palomena pr
31	18	22.2	10	1	BPP_VIPAS	P31351	vipera aspi
32	18	22.2	13	1	MP1_MICOC	P81532	microplitis
33	18	22.2	17	1	H2B3 ICTPU	P81904	ictalurus p
34	17	21.0	10	1	BPP2_BOTIN	P30422	bothrops in
35	17	21.0	10	1	BPP2_BOTJA	P01022	bothrops ja
36	17	21.0	11	1	TKN4_PSEGU	P42989	pseudophryn
37	17	21.0	11	1	TKN5_PSEGU	P42990	pseudophryn
38	17	21.0	12	1	TKN1_KASMA	P08613	kassina mac
39	17	21.0	13	1	BRK_PARID	P42717	parapolybia
40	17	21.0	13	1	GER1_HORVU	P28525	hordeum vul
41	17	21.0	13	1	GER2_HORVU	P28526	hordeum vul
42	17	21.0	14	1	PH1_PRUSE	P29263	prunus sero
43	17	21.0	14	1	TAT_HV1W2	P12509	human immun
44	17	21.0	14	1	TAT_HV1Z8	P12511	human immun
45	17	21.0	15	1	AF1L_MALPA	P83141	malva parvi
46	17	21.0	15	1	AFP3_MALPA	P83137	malva parvi
47	17	21.0	15	1	CXA2_CONAL	P56640	conus aulic
48	17	21.0	15	1	NUO8_SOLTU	P80731	solanum tub
49	17	21.0	15	1	PH3_PRUSE	P29265	prunus sero
50	17	21.0	16	1	CXA1_CONAL	P56639	conus aulic
51	17	21.0	16	1	CXA3_CONAL	P56641	conus aulic
52	17	21.0	16	1	PH2_PRUSE	P29264	prunus sero
53	17	21.0	17	1	TL09_SPIOL	P82671	spinacia ol
54	17	21.0	17	1	YALA_TRYBB	P17961	trypanosoma
55	16	19.8	8	1	HTF_TENMO	P25419	tenebrio mo
56	16	19.8	8	1	RPCH_PANBO	P08939	pandalus bo
57	16	19.8	9	1	YBFR_AZOVI	P25825	azotobacter
58	16	19.8	10	1	BRK_ONCMY	Q9prz1	oncorhynchu
59	16	19.8	10	1	UPA8_HUMAN	P30094	homo sapien
60	16	19.8	10	1	XYNB_DICB4	P80717	dictyoglomu
61	16	19.8	13	1	IDHA_CANFA	P54836	canis famil
62	16	19.8	13	1	LMT4_LOCFI	P41490	locusta mig
63	16	19.8	13	1	NO40_PEA	P55959	pisum sativ
64	16	19.8	13	1	UHA3_CANFA	P56535	canis famil
65	16	19.8	15	1	AH2_PRUSE	P29260	prunus sero
66	16	19.8	15	1	ESTJ_MANSE	P19985	manduca sex
67	16	19.8	15	1	UC25_MAIZE	P80631	zea mays (m
68	16	19.8	16	1	AF1S_MALPA	P83140	malva parvi
69	16	19.8	16	1	AH1_PRUSE	P29259	prunus sero
70	16	19.8	16	1	MMPX_SOLTU	P80501	solanum tub
71	16	19.8	17	1	PSBL_SYNVU	P12241	synechococc
72	16	19.8	18	1	LUXB_KRYAS	P18300	kryptophana
73	16	19.8	18	1	RL24_PROVU	P20032	proteus vul
74	15	18.5	8	1	AKH_LIBAU	P25418	libellula a

75	15	18.5	8	1	AKH_TABAT	P14595	tabanus atr
76	15	18.5	8	1	ALL5_CALVO	P41841	calliphora
77	15	18.5	8	1	HTF1_PERAM	P04548	periplaneta
78	15	18.5	8	1	HTF2_PERAM	P04549	periplaneta
79	15	18.5	8	1	RS7_MYCIT	P33564	mycobacteri
80	15	18.5	9	1	SAP_STOVA	P24047	stomopneute
81	15	18.5	10	1	COXQ_SHEEP	P80337	ovis aries
82	15	18.5	10	1	HTF1_ROMMI	P18110	romalea mic
83	15	18.5	10	1	HTF2_CARMO	P11385	carausius m
84	15	18.5	10	1	HTF_NAUCI	P10939	nauphoeta c
85	15	18.5	10	1	HTF_TABAT	P14596	tabanus atr
86	15	18.5	11	1	EFG_CLOPA	P81350	clostridium
87	15	18.5	11	1	Q2OA_COMTE	P80464	comamonas t
88	15	18.5	11	1	TKNA_ONCMY	P28499	oncorhynch
89	15	18.5	11	1	TKNA_SCYCA	P41333	scyliorhinu
90	15	18.5	13	1	BPP1_BOTJA	P01020	bothrops ja
91	15	18.5	13	1	LIGA_TRAVE	P20011	trametes ve
92	15	18.5	14	1	MCRZ_METTM	P58816	methanobact
93	15	18.5	15	1	ATP2_PINPS	P81663	pinus pinas
94	15	18.5	15	1	IRBP_CRISP	P12665	cricetidae
95	15	18.5	15	1	UC06_MAIZE	P80612	zea mays (m
96	15	18.5	15	1	UE15_HORVU	P34938	hordeum vul
97	15	18.5	15	1	URE2_MORMO	P17338	morganella
98	15	18.5	16	1	FOR2_MYRGU	P81437	myrmecia gu
99	15	18.5	16	1	PPAC_BACME	P56948	bacillus me
100	15	18.5	16	1	RBL_CAPAN	P27063	capsicum an

# ALIGNMENTS

## RESULT 1

### PRP\_MYCBO

ID PRP\_MYCBO STANDARD; PRT; 15 AA.  
AC P80149;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE Proline-rich protein (Fragment).  
OS Mycobacterium bovis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1765;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=BCG / Paris 1173 P2;  
RX MEDLINE=93281750; PubMed=8506381;  
RA Romain F., Augier J., Pescher P., Marchal G.A.;  
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-  
RT type hypersensitivity reactions only in guinea pigs immunized with  
RT living mycobacteria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY  
CC REACTIONS IN GUINEA PIGS.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 40.7%; Score 33; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|||||  
Db 7 PPPPQ 11

RESULT 2

TMOF\_AEDAE

ID TMOF\_AEDAE STANDARD; PRT; 10 AA.  
AC P19425;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
OX NCBI\_TaxID=7159;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;  
RX MEDLINE=90367888; PubMed=2394318;  
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
RT "Mosquito oostatic factor: a novel decapeptide modulating  
RT trypsin-like enzyme biosynthesis in the midgut.";  
RL FASEB J. 4:3015-3020(1990).  
RN [2]  
RP SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;  
RX MEDLINE=93357794; PubMed=8353526;  
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
RT "Mass spectrometry and characterization of Aedes aegypti trypsin  
RT modulating oostatic factor (TMOF) and its analogs.";  
RL Insect Biochem. Mol. Biol. 23:703-712(1993).  
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis  
CC in the midgut which indirectly reduces the vitellogenin  
CC concentration in the hemolymph resulting in inhibition of oocyte  
CC development.  
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular  
CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at  
CC 36 hrs and stops at 56 hrs.  
DR PIR; A36454; A36454.  
KW Hormone.  
FT DOMAIN 3 10 POLY-PRO.  
FT VARIANT 1 2 YD -> DY (IN TMFO(B)).  
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 34.6%; Score 28; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10  
|||||

## RESULT 3

## IBP4\_PIG

ID IBP4\_PIG STANDARD; PRT; 16 AA.  
AC P24854;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)  
DE (IGF-binding protein 4) (Fragment).  
GN IGFBP4.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92109718; PubMed=1722398;  
RA Coleman M.E., Pan Y.-C.E., Etherton T.D.;  
RT "Identification and NH2-terminal amino acid sequence of three  
RT insulin-like growth factor-binding proteins in porcine serum."  
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).  
CC -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs  
CC and have been shown to either inhibit or stimulate the growth  
CC promoting effects of the IGFs on cell culture. They alter the  
CC interaction of IGFs with their cell surface receptors.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Contains 1 IGFBP domain.  
CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
DR PIR; JH0517; JH0517.  
DR InterPro; IPR000867; Insl\_gro\_fac\_pr.  
DR InterPro; IPR000716; Thyroglobulin\_1.  
DR PROSITE; PS00222; IGF\_BINDING; PARTIAL.  
DR PROSITE; PS00484; THYROGLOBULIN\_1; PARTIAL.  
KW Growth factor binding.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 33.3%; Score 27; DB 1; Length 16;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
||| :|  
Db 7 PPPSEE 12

## RESULT 4

## BPP3\_BOTIN

ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
AC P30423;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting

DE enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8723;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating

RT peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

DR PIR; C37196; C37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 29.6%; Score 24; DB 1; Length 11;

Best Local Similarity 80.0%; Pred. No. 4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11

|||

Db 4 PPRPQ 8

# RESULT 5

## BPP4\_BOTIN

ID BPP4\_BOTIN STANDARD; PRT; 11 AA.

AC P30424;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting

DE enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8723;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating

RT peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.  
DR PIR; D37196; D37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 29.6%; Score 24; DB 1; Length 11;  
Best Local Similarity 80.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|| ||  
Db 4 PPRPQ 8

#### RESULT 6

##### Q2OB\_COMTE

ID Q2OB\_COMTE STANDARD; PRT; 10 AA.  
AC P80465;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).  
OS Comamonas testosteroni (Pseudomonas testosteroni).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Comamonas.  
OX NCBI\_TaxID=285;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=63;  
RX MEDLINE=96035889; PubMed=7556204;  
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
RT quinoline and 3-methylquinoline degradation.";  
RL Eur. J. Biochem. 232:536-544(1995).  
CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)-2-oxo-1,2-  
CC dihydroquinoline.  
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-  
CC 1(2H)-one + reduced acceptor.  
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.  
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first  
CC step.  
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and  
CC two gamma chains (Probable).  
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 28.4%; Score 23; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFP 7  
||||  
Db 1 MKFP 4

# RESULT 7

## TY13\_PHYRO

ID TY13\_PHYRO STANDARD; PRT; 13 AA.  
 AC P04096;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-13.  
 OS Phyllomedusa rohdei (Rohde's leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Phyllomedusinae; Phyllomedusa.  
 OX NCBI\_TaxID=8394;  
 RN [1]  
 RP SEQUENCE.  
 RA Montecucchi P.C., Gozzini L., Erspamer V.;  
 RT "Primary structure determination of a tryptophan-containing  
 RT tridecapeptide from Phyllomedusa rohdei."  
 RL Int. J. Pept. Protein Res. 27:175-182(1986).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 DR PIR; A05174; A05174.  
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 28.4%; Score 23; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 6.7e+02;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMKFPPPP 10  
 | : |||  
 Db 2 EKPYPWPPP 9

# RESULT 8

## CPAX\_BOVIN

ID CPAX\_BOVIN STANDARD; PRT; 18 AA.  
 AC P22779;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91027757; PubMed=2121272;  
 RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;  
 RT "Identification and biochemical analysis of novel olfactory-specific  
 RT cytochrome P-450IIA and UDP-glucuronosyl transferase."  
 RL Biochemistry 29:7433-7440(1990).  
 CC -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate



CC monooxygenases. In liver microsomes, this enzyme is involved in an  
 CC NADPH-dependent electron transport pathway. It oxidizes a variety  
 CC of structurally unrelated compounds, including steroids, fatty  
 CC acids, and xenobiotics.  
 CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -!- SIMILARITY: Belongs to the cytochrome P450 family.  
 DR PIR; A35704; A35704.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; PARTIAL.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum; Olfaction.  
 FT NON\_TER 1 1  
 FT VARIANT 6 6 G -> D.  
 FT VARIANT 11 11 A -> E.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 28.4%; Score 23; DB 1; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 9.4e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
 | : | ||:  
 Db 1 MXYLPGPQQ 9

#### RESULT 9

##### FIF1\_SARBU

ID FIF1\_SARBU STANDARD; PRT; 12 AA.  
 AC P83349;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neb-FIRFamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE=CNS;  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
 RT "Identification in Drosophila melanogaster of the invertebrate G  
 RT protein-coupled FMRFamide receptor."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
 CC junctions.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 12 12 AMIDATION.

SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 27.2%; Score 22; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12

|||:

Db 2 PPQPSD 7

#### RESULT 10

##### HS9A\_RAT

ID HS9A\_RAT STANDARD; PRT; 12 AA.  
AC P82995;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Heat shock protein HSP 90-alpha (Fragment).  
GN HSPCA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=21589773; PubMed=11732320;  
RA Langer T., Fasold H.;  
RT "Isolation and quantification of the heat shock protein 90 alpha and  
RT beta isoforms from rat liver."  
RL Protoplasma 218:54-56(2001).  
CC -!- FUNCTION: Molecular chaperone. Has ATPase activity (By  
CC similarity).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the heat shock protein 90 family.  
DR InterPro; IPR001404; Hsp90.  
DR PROSITE; PS00298; HSP90; PARTIAL.  
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.  
FT MOD\_RES 4 4 PHOSPHORYLATION (BY DS-DNA KINASE) (BY  
FT SIMILARITY).  
FT MOD\_RES 6 6 PHOSPHORYLATION (BY DS-DNA KINASE) (BY  
FT SIMILARITY).  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 27.2%; Score 22; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 8.6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 PQETVT 15

|:|||

Db 1 PEETQT 6

#### RESULT 11

# LEC\_DELRE

ID LEC\_DELRE STANDARD; PRT; 16 AA.  
AC P83511;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Lectin (DRL) (Fragment).  
OS Delonix regia (Royal poinciana).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Caesalpinioideae; Caesalpinieae;  
OC Delonix.  
OX NCBI\_TaxID=72433;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC TISSUE=Seed;  
RX MEDLINE=22158378; PubMed=12168698;  
RA Pando S.C., Macedo M.L.R., Freire M.G.M., Toyama M.H., Novello J.C.,  
RA Marangoni S.;  
RT "Biochemical characterization of a lectin from Delonix regia seeds.";  
RL J. Protein Chem. 21:279-285(2002).  
CC -!- FUNCTION: Glucose-specific lectin.  
CC -!- SUBUNIT: Monomer.  
CC -!- MISCELLANEOUS: Optimal pH is 8.0-9.0. Active up to 60 degrees  
CC Celsius.  
CC -!- MISCELLANEOUS: Requires manganese but not calcium ions for cell-  
CC agglutinating activity.  
CC -!- SIMILARITY: Belongs to the leguminous lectin family.  
DR GO; GO:0005536; F:glucose binding; IDA.  
DR GO; GO:0030145; F:manganese ion binding; IDA.  
DR GO; GO:0016337; P:cell-cell adhesion; IDA.  
DR InterPro; IPR001220; Lectin\_legB.  
DR PROSITE; PS00307; LECTIN\_LEGUME\_BETA; PARTIAL.  
KW Lectin; Glycoprotein; Manganese.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1816 MW; D3DA3A36D1C308BE CRC64;

Query Match 27.2%; Score 22; DB 1; Length 16;  
Best Local Similarity 40.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 KFPPPPQETV 14  
| | | | :  
Db 4 KFPKDQQLI 13

## RESULT 12

### APID\_BOMPA

ID APID\_BOMPA STANDARD; PRT; 17 AA.  
AC P81464;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Apidaecin.  
OS Bombus pascuorum (Brown bumble bee).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

OC Apidae; Bombus.  
 OX NCBI\_TaxID=65598;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=97362903; PubMed=9219367;  
 RA Rees J.A., Moniatte M., Bulet P.;  
 RT "Novel antibacterial peptides isolated from a European bumblebee,  
 RT Bombus pascuorum (Hymenoptera, Apoidea).";  
 RL Insect Biochem. Mol. Biol. 27:413-422(1997).  
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.  
 CC -!- INDUCTION: By bacterial infection.  
 DR InterPro; IPR004828; Apidaecin.  
 DR Pfam; PF00807; Apidaecin; 1.  
 KW Insect immunity; Antibiotic; Hemolymph.  
 SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 27.2%; Score 22; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPQ 11  
 |||:  
 Db 8 PPPR 11

# RESULT 13

## URE3\_MORMO

ID URE3\_MORMO STANDARD; PRT; 10 AA.  
 AC P17339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)  
 DE (Urease 6 kDa subunit) (Fragment).  
 GN UREA.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the urease gamma subunit family.  
 DR PIR; C35389; C35389.  
 DR HAMAP; MF\_00739; -; 1.  
 KW Hydrolase.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 10;  
Best Local Similarity 44.4%; Pred. No. 9.9e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12  
|: || |  
Db 1 MQLTPPEVE 9

RESULT 14

SODM\_STRGR

ID SODM\_STRGR STANDARD; PRT; 15 AA.  
AC P80733;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).  
GN SOD2.  
OS Streptomyces griseus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1911;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=KCTC 9006;  
RX MEDLINE=97056064; PubMed=8900409;  
RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,  
RA Kang S.-O.;  
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus."  
RL Arch. Biochem. Biophys. 334:341-348(1996).  
CC -!- FUNCTION: Destroys radicals which are normally produced within the  
CC cells and which are toxic to biological systems.  
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
CC -!- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).  
CC -!- SUBUNIT: Tetramer.  
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
CC family.  
DR InterPro; IPR001189; SODismutase.  
DR Pfam; PF00081; sodfe; 1.  
DR PROSITE; PS00088; SOD\_MN; PARTIAL.  
KW Oxidoreductase; Metal-binding; Iron; Zinc.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
| || :  
Db 6 PEPPYD 11

RESULT 15

UF04\_MOUSE

ID UF04\_MOUSE STANDARD; PRT; 7 AA.

AC P38642;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familiar and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis."  
 RL Electrophoresis 15:735-745(1994).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.0, its MW is: 46 kDa.  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 PPPP 10  
 | ||  
 Db 1 PKPP 4

# RESULT 16

## BPPB\_AGKHA

ID BPPB\_AGKHA STANDARD; PRT; 11 AA.  
 AC P01021;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide B (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 OX NCBI\_TaxID=242054;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Kato H., Suzuki T.;  
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from  
 RT the venom of Agkistrodon halys blomhoffii."  
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01254; XASNBA.

KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
|||:  
Db 4 PPRPK 8

#### RESULT 17

TKNA\_GADMO

ID TKNA\_GADMO STANDARD; PRT; 11 AA.

AC P28498;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P.

OS Gadus morhua (Atlantic cod).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.

OX NCBI\_TaxID=8049;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;

RT "Substance-P-related and neurokinin-A-related peptides from the brain  
of the cod and trout.";

RL Eur. J. Biochem. 206:659-664(1992).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S23306; S23306.

DR InterPro; IPR002040; Tachy\_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).

SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 11;  
Best Local Similarity 42.9%; Pred. No. 1.5e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PPPQETV 14  
| ||: :  
Db 2 PRPQQFI 8

# RESULT 18

## TKNA\_HORSE

ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
AC P01290;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
GN TAC1 OR NKNA OR TAC2 OR NKA.  
OS Equus caballus (Horse), and  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796, 10141;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Horse;  
RA Studer R.O., Trzeciak A., Lergier W.;  
RT "Isolation and amino-acid sequence of substance P from horse  
RT intestine.";  
RL Helv. Chim. Acta 56:860-866(1973).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C.porcellus;  
RX MEDLINE=90044685; PubMed=2478925;  
RA Murphy R.;  
RT "Primary amino acid sequence of guinea-pig substance P.";  
RL Neuropeptides 14:105-110(1989).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A01558; SPHO.  
DR PIR; A60654; A60654.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPPQE 12  
| | |:  
Db 2 PKPQQ 6

# RESULT 19



## TKN2\_KASMA

ID TKN2\_KASMA STANDARD; PRT; 12 AA.  
 AC P08614;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hylambatin.  
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
 OC Kassina.  
 OX NCBI\_TaxID=8414;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
 RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and  
 RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
 RT maculatus.";  
 RL Biomed. Res. 2:613-617(1981).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S07436; S07436.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPP 10  
 |||  
 Db 2 PPDP 5

## RESULT 20

## AF2S\_MALPA

ID AF2S\_MALPA STANDARD; PRT; 16 AA.  
 AC P83142;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).  
 OS Malva parviflora (Little mallow) (Cheeseweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;

RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (*Malva parviflora*).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
 CC -!- FUNCTION: Possesses antifungal activity against *P.infestans* but not *F.graminearum*.  
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt concentration.  
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
 KW Fungicide; Antibiotic.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7EE65 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPQE 12  
 |||:  
 Db 9 PPQK 12

#### RESULT 21

##### A45K\_MYCBO

ID A45K\_MYCBO STANDARD; PRT; 17 AA.  
 AC P80069;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 45/47 kDa antigen (Fragment).  
 OS *Mycobacterium bovis*.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=BCG / Paris 1173 P2;  
 RX MEDLINE=93138802; PubMed=8423100;  
 RA Romain F., Laqueyrie A., Militzer P., Pescher P., Chavarot P.,  
 RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;  
 RT "Identification of a *Mycobacterium bovis* BCG 45/47-kilodalton antigen complex, an immunodominant target for antibody response after immunization with living bacteria.";  
 RL Infect. Immun. 61:742-750(1993).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.  
 DR PIR; A49237; A49237.  
 KW Antigen.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPP 10  
| |  
Db 4 PAPP 7

RESULT 22

UPA2\_HUMAN

ID UPA2\_HUMAN STANDARD; PRT; 10 AA.  
AC P30088;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing";  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 4.4, its MW is: 49 kDa.  
DR SWISS-2DPAGE; P30088; HUMAN.  
FT NON\_TER 1 1  
FT UNSURE 6 6  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PPQETV 14  
| | : |  
Db 5 PPDDQV 10

RESULT 23

BPP\_AGKHP

ID BPP\_AGKHP STANDARD; PRT; 11 AA.  
AC P04562;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys  
OS pallas).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 OX NCBI\_TaxID=8714;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=86177022; PubMed=3008123;  
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
 RT "Structure-function studies on the bradykinin potentiating peptide  
 RT from Chinese snake venom (*Agkistrodon halys pallas*).";  
 RL Peptides 6 Suppl. 3:339-342(1985).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; JC0002; XAVIBH.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPP 10  
 |||  
 Db 4 PPGP 7

#### RESULT 24

TKN1\_PSEGU  
 ID TKN1\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42986;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-I (PG-KI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guentheri*.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; B60409; B60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 PPPQETV 14  
 | | | |  
 Db 2 PHPDEFV 8

# RESULT 25

## TKN2\_PSEGU

ID TKN2\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42987;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (PG-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; C60409; C60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation; .  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPPQETV 14  
 | | | |  
 Db 2 PNPDEFV 8

# RESULT 26

## TKN3\_PSEGU

ID TKN3\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42988;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-III (PG-KIII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 2.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PPPQETV 14  
| | | |  
Db 2 PHPNEFV 8

RESULT 27

TKNA\_CHICK

ID TKNA\_CHICK STANDARD; PRT; 11 AA.  
AC P19850;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=88204263; PubMed=2452461;  
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";  
RL Regul. Pept. 20:171-180(1988).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; JN0023; JN0023.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPPQE 12  
| ||:  
Db 2 PRPQQ 6

RESULT 28

LPER\_BACLI

ID LPER\_BACLI STANDARD; PRT; 14 AA.  
AC Q04303;  
DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Erythromycin resistance leader peptide (23S rRNA methylase leader  
 DE peptide).  
 OS *Bacillus licheniformis*, and  
 OS *Bacillus anthracis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=1402, 1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*B.licheniformis*;  
 RX MEDLINE=84245158; PubMed=6429477;  
 RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;  
 RT "DNA sequence and regulation of *ermD*, a macrolide-lincosamide-  
 RT streptogramin B resistance element from *Bacillus licheniformis*.";  
 RL Mol. Gen. Genet. 194:349-356(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*B.licheniformis*; STRAIN=EMR-1;  
 RX MEDLINE=91310580; PubMed=1713206;  
 RA Kwak J.-K., Choi E.-C., Weisblum B.;  
 RT "Transcriptional attenuation control of *ermK*, a  
 RT macrolide-lincosamide-streptogramin B resistance determinant from  
 RT *Bacillus licheniformis*.";  
 RL J. Bacteriol. 173:4725-4735(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*B.anthraxis*; STRAIN=590;  
 RX MEDLINE=93232776; PubMed=8473865;  
 RA Kim H.-S., Choi E.-C., Kim B.-K.;  
 RT "A macrolide-lincosamide-streptogramin B resistance determinant from  
 RT *Bacillus anthracis* 590: cloning and expression of *ermJ*.";  
 RL J. Gen. Microbiol. 139:601-607(1993).  
 CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF  
 CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B  
 CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L08389; AAA22596.1; -.  
 DR EMBL; M29832; AAA22598.1; -.  
 DR PIR; A42473; A42473.  
 KW Antibiotic resistance; Leader peptide.  
 SQ SEQUENCE 14 AA; 1732 MW; 5D1138B59F32ED07 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 14;  
 Best Local Similarity 33.3%; Pred. No. 2.7e+03;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LEMKFP 7  
 : ::||



## RESULT 29

## MARI\_ALTSP

ID MARI\_ALTSP STANDARD; PRT; 14 AA.  
 AC P29399;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Marinostatin C-2 [Marinostatin C-1; Marinostatin D].  
 OS Alteromonas sp. (strain B-10-31).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Alteromonas.  
 OX NCBI\_TaxID=29456;  
 RN [1]  
 RP SEQUENCE, AND ACTIVE SITE.  
 RX MEDLINE=92176155; PubMed=1794974;  
 RA Takano R., Imada C., Kamei K., Hara S.;  
 RT "The reactive site of marinostatin, a proteinase inhibitor from  
 RT marine Alteromonas sp. B-10-31.";  
 RL J. Biochem. 110:856-858(1991).  
 CC -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT  
 CC NOT TRYPSIN.  
 KW Serine protease inhibitor; Pyrrolidone carboxylic acid.  
 FT PEPTIDE 1 14 MARINOSTATIN C-2.  
 FT PEPTIDE 3 14 MARINOSTATIN C-1.  
 FT PEPTIDE 4 14 MARINOSTATIN D.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 6 7 REACTIVE BOND.  
 SQ SEQUENCE 14 AA; 1644 MW; 6E7CEE92EF32E44 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 14;

Best Local Similarity 33.3%; Pred. No. 2.7e+03;

Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MKFPPPPQE 12

|::| |

Db 6 MRYPSSDSE 14

## RESULT 30

## MK1\_PALPR

ID MK1\_PALPR STANDARD; PRT; 15 AA.  
 AC P80408;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metalnikowin I.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Hemolymph;  
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.  
 CC -!- INDUCTION: By bacterial infection.  
 KW Antibiotic; Insect immunity.  
 SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PPPP 10  
 | ||  
 Db 10 PRPP 13

# RESULT 31

## BPP\_VIPAS

ID BPP\_VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y., Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting  
 RT enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KFPP 8

Db                    | ||  
7 KVPP 10

RESULT 32

MP1\_MICOC

ID MP1\_MICOC            STANDARD;            PRT;       13 AA.  
AC P81532;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE MP1 protein (Fragments).  
OS Microplitis ocellatae (Braconid wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;  
OC Braconidae; Microgastrinae; Microplitis.  
OX NCBI\_TaxID=99573;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RA Takahashi M., Quicke D.L.J.;  
RL Submitted (OCT-1998) to Swiss-Prot.  
CC -!- TISSUE SPECIFICITY: Salivary glands.  
CC -!- DEVELOPMENTAL STAGE: LARVAL.  
FT NON\_CONS       10       11  
SQ SEQUENCE       13 AA;    1595 MW;    0C0786C9DD82777B CRC64;

Query Match                    22.2%;    Score 18;    DB 1;    Length 13;  
Best Local Similarity       75.0%;    Pred. No. 3.5e+03;  
Matches       3;    Conservative       0;    Mismatches       1;    Indels       0;    Gaps       0;

Qy                    7 PPPP 10  
                      | ||  
Db                    5 PYPP 8

RESULT 33

H2B3\_ICTPU

ID H2B3\_ICTPU            STANDARD;            PRT;       17 AA.  
AC P81904;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Histone H2B-3 (Antibacterial histone-like protein 3) (HLP-3)  
DE (Fragment).  
OS Ictalurus punctatus (Channel catfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;  
OC Ictaluridae; Ictalurus.  
OX NCBI\_TaxID=7998;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Skin;  
RX MEDLINE=98309109; PubMed=9645227;  
RA Robinette D., Wada S., Arroll T., Levy M.G., Miller W.L., Noga E.J.;  
RT "Antimicrobial activity in the skin of the channel catfish Ictalurus  
punctatus: characterization of broad-spectrum histone-like

RT antimicrobial proteins.";  
 RL Cell. Mol. Life Sci. 54:467-475(1998).  
 CC -!- FUNCTION: Has antimicrobial activity. Possesses strong activity  
 CC against saprolegnia, the most common fungal infection in fish.  
 CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules  
 CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146  
 CC bp of DNA.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- MASS SPECTROMETRY: MW=13506; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the histone H2B family.  
 DR InterPro; IPR000558; Histone\_H2B.  
 DR PROSITE; PS00357; HISTONE\_H2B; PARTIAL.  
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;  
 KW Antibiotic; Fungicide.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1795 MW; 44FB8D966FD2F377 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PPPQET 13  
 | | : |  
 Db 1 PDPAKT 6

#### RESULT 34

##### BPP2\_BOTIN

ID BPP2\_BOTIN STANDARD; PRT; 10 AA.  
 AC P30422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPPQ 11  
| ||  
Db 4 PHPQ 7

RESULT 35

BPP2\_BOTJA

ID BPP2\_BOTJA STANDARD; PRT; 10 AA.  
AC P01022;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).  
DE  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=72118526; PubMed=4334402;  
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,  
RA Kocy O.;  
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
RT jararaca. Isolation, elucidation of structure, and synthesis."  
RL Biochemistry 10:4033-4039(1971).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01255; XAVI6B.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PPPQ 11  
| ||  
Db 4 PRPQ 7

RESULT 36

TKN4\_PSEGU

ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
AC P42989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide I (PG-SPI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; E60409; E60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PPPQE 12  
 | | |  
 Db 2 PNPDE 6

#### RESULT 37

TKN5\_PSEGU

ID TKN5\_PSEGU STANDARD; PRT; 11 AA.

AC P42990;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide II (PG-SPII).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI\_TaxID=30349;

RN [1]

RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; F60409; F60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PPPQE 12  
 | | |  
 Db 2 PNPNE 6

#### RESULT 38

##### TKN1\_KASMA

ID TKN1\_KASMA STANDARD; PRT; 12 AA.  
 AC P08613;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hylambates kassinin ([Glu2,Pro5]kassinin).  
 OS Kassina maculata (African rhacophorid frog) (*Hylambates maculatus*).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
 OC Kassina.  
 OX NCBI\_TaxID=8414;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
 RT "New tachykinins, Glu2, Pro5-kassinin (*hylambates*-kassinin) and  
 RT hylambatin, in the skin of the African rhacophorid frog *Hylambates*  
 RT *maculatus*.";  
 RL Biomed. Res. 2:613-617(1981).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S10059; S10059.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
 | | |  
 Db 3 PKPDQ 7

#### RESULT 39

##### BRK\_PARID

ID BRK\_PARID STANDARD; PRT; 13 AA.  
 AC P42717;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Waspkinin.  
 OS Parapolybia indica.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Polistinae; Parapolybia.  
 OX NCBI\_TaxID=31921;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Toki T., Yasuhara T., Nakajima T.;  
 RT "Isolation and sequential analysis of peptides on the venom sac of  
 RT Parapolybia indica.";  
 RL Eisei Dobutsu 39:105-111(1988).  
 CC -!- FUNCTION: Induces smooth muscle contraction.  
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
 CC -!- SIMILARITY: Belongs to the bradykinin family.  
 KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;



Qy 3 EMKFPP 8  
: | |  
Db 1 QZKRPP 6

RESULT 40

GER1\_HORVU

ID GER1\_HORVU STANDARD; PRT; 13 AA.  
AC P28525;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Germin GS1 (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. CM 72; TISSUE=Root;  
RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
RT "Germin-like polypeptides increase in barley roots during salt  
RT stress.";  
RL Plant Physiol. 97:366-374(1991).  
CC -!- FUNCTION: May play a role in altering the properties of cell  
CC walls during germinative growth.  
CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
CC (By similarity).  
CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in  
CC the mature region, but not in the tip. Not detected in leaves.  
CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
CC stress in coleoptile.  
CC -!- PTM: Glycosylated.  
CC -!- SIMILARITY: Belongs to the germin family.  
DR InterPro; IPR001929; Germin.  
DR PROSITE; PS00725; GERMIN; PARTIAL.  
KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
FT UNSURE 10 10  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7B6D7 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
| | |:  
Db 3 PSPLQD 8

RESULT 41

GER2\_HORVU

ID GER2\_HORVU STANDARD; PRT; 13 AA.  
AC P28526;  
DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS2 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress.";  
 RL Plant Physiol. 97:366-374(1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell walls  
 CC during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the  
 CC mature region, but not in the tip. Not detected in leaves.  
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
 CC stress in coleoptile.  
 CC -!- PTM: Glycosylated.  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
 | | |:  
 Db 3 PSPLQD 8

#### RESULT 42

##### PH1\_PRUSE

ID PH1\_PRUSE STANDARD; PRT; 14 AA.  
 AC P29263;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase  
 DE isozyme I) (PH I) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
 CC glucose.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits  
 CC until 6 weeks after flowering. Then, concomitant with cotyledon  
 CC development, the level of enzyme increases with specificity for  
 CC embryonal tissues.  
 CC -!- PTM: Glycosylated.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1575 MW; FB3D7F4FB90CA9CA CRC64;

Query Match 21.0%; Score 17; DB 1; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 5.2e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPP 8  
 :||  
 Db 2 YPP 4

#### RESULT 43

TAT\_HV1W2

ID TAT\_HV1W2 STANDARD; PRT; 14 AA.  
 AC P12509;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE TAT protein (Transactivating regulatory protein) (Fragment).  
 GN TAT.  
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11705;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86235450; PubMed=3012778;  
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,  
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;  
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or  
 RT at risk for AIDS.";  
 RL Science 232:1548-1553(1986).  
 CC -!- FUNCTION: Transcriptional regulator that acts by binding to the  
 CC trans-activating responsive sequence (TAR) RNA element and  
 CC activates transcription initiation and/or elongation from the LTR  
 CC promoter.  
 CC -!- SUBUNIT: Binds cyclin T1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
 CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM  
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
 CC WAS PERINATALLY INFECTED BY HER MOTHER.  
 CC -----  
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CC -----

DR EMBL; M12507; AAB12991.1; -.  
DR HIV; M12507; TAT\$WMJ2.  
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
KW AIDS.  
FT NON\_TER 1 1  
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BFEF67AA8 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
| |:  
Db 9 PTGPKE 14

#### RESULT 44

TAT\_HV128

ID TAT\_HV128 STANDARD; PRT; 14 AA.  
AC P12511;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE TAT protein (Transactivating regulatory protein) (Fragment).  
GN TAT.  
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11681;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88281278; PubMed=3395517;  
RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,  
RA Gallo R.C.;  
RT "Nucleotide sequence analysis of the env gene of a new Zairian  
RT isolate of HIV-1.";  
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).  
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the  
CC trans-activating responsive sequence (TAR) RNA element and  
CC activates transcription initiation and/or elongation from the LTR  
CC promoter.  
CC -!- SUBUNIT: Binds cyclin T1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
CC ZAIREAN MALE.  
CC -----

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CC -----

DR EMBL; J03653; AAA44685.1; -.  
DR HIV; J03653; TAT\$JY1.  
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
KW AIDS.  
FT NON\_TER 1 1  
SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQE 12  
| |:  
Db 9 PTGPKE 14

#### RESULT 45

##### AF1L\_MALPA

ID AF1L\_MALPA STANDARD; PRT; 15 AA.  
AC P83141;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Antifungal protein 1 large subunit (CW-1) (Fragment).  
OS Malva parviflora (Little mallow) (Cheeseweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
OX NCBI\_TaxID=145753;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Seed;  
RX MEDLINE=20568734; PubMed=11118343;  
RA Wang X., Bunkers G.J.;  
RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
RT parviflora).";  
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
CC not F.graminearum.  
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
CC concentration.  
DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
KW Fungicide; Antibiotic.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1783 MW; 2CB3079F53CC70F9 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;  
Best Local Similarity 37.5%; Pred. No. 5.6e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KFPPPPQE 12  
: || :  
Db 6 RIPPLRRE 13

# RESULT 46

## AFP3\_MALPA

ID AFP3\_MALPA STANDARD; PRT; 15 AA.  
AC P83137;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Antifungal protein 3 (CW-3) (Fragment).  
OS Malva parviflora (Little mallow) (Cheeseweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
OX NCBI\_TaxID=145753;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Seed;  
RX MEDLINE=21199399; PubMed=11302747;  
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;  
RT "Purification and characterization of three antifungal proteins from  
RT cheeseweed (Malva parviflora).";  
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).  
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
CC not F.graminearum.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
CC concentration.  
DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
DR GO; GO:0007275; P:development; NAS.  
KW Fungicide; Antibiotic.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 PPPPQ 11  
| ||  
Db 1 PEDPQ 5

# RESULT 47

## CXA2\_CONAL

ID CXA2\_CONAL STANDARD; PRT; 15 AA.  
AC P56640;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Alpha-conotoxin AuIB.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]

RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99003392; PubMed=9786965;  
RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
RA Olivera B.M., McIntosh J.M.;  
RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic  
RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
RL J. Neurosci. 18:8571-8579(1998).  
RN [2]  
RP STRUCTURE BY NMR.  
RX MEDLINE=20187585; PubMed=10722709;  
RA Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.;  
RT "Nuclear magnetic resonance solution conformation of alpha-conotoxin  
RT AuIB, an alpha(3)beta(4) subtype-selective neuronal nicotinic  
RT acetylcholine receptor antagonist.";  
RL J. Biol. Chem. 275:8680-8685(2000).  
RN [3]  
RP STRUCTURE BY NMR.  
RX MEDLINE=22359066; PubMed=12376538;  
RA Dutton J.L., Bansal P.S., Hogg R.C., Adams D.J., Alewood P.F.,  
RA Craik D.J.;  
RT "A new level of conotoxin diversity, a non-native disulfide bond  
RT connectivity in alpha-conotoxin AuIB reduces structural definition  
RT but increases biological activity.";  
RL J. Biol. Chem. 277:48849-48857(2002).  
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
CC inhibit them. This peptide blocks mammalian nicotinic  
CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
CC family.  
DR PDB; 1DG2; 23-MAY-00.  
DR PDB; 1MXN; 30-DEC-02.  
DR PDB; 1MXP; 30-DEC-02.  
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
FT DISULFID 2 8  
FT DISULFID 3 15  
FT MOD\_RES 15 15 AMIDATION.  
SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 5.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPP 8  
:|  
Db 5 YPP 7

RESULT 48  
NUO8\_SOLTU  
ID NUO8\_SOLTU STANDARD; PRT; 15 AA.  
AC P80731;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 12 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Complex I-12KD) (CI-12KD) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Bintje; TISSUE=Tuber;  
 RA Herz U., Grohmann L.;  
 RL Submitted (DEC-1996) to Swiss-Prot.  
 CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory  
 CC chain. The immediate electron acceptor for the enzyme is believed  
 CC to be ubiquinone.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- SUBUNIT: Complex I is composed of about 30 different subunits.  
 CC -!- SUBCELLULAR LOCATION: Matrix side of the mitochondrial inner  
 CC membrane.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1668 MW; EDC87B30AD155854 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MKFPP 8  
 | ||  
 Db 7 MXVPP 11

#### RESULT 49

##### PH3\_PRUSE

ID PH3\_PRUSE STANDARD; PRT; 15 AA.  
 AC P29265;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase  
 DE isozyme IIB) (PH IIB) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-



CC glucose.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits  
 CC until 6 weeks after flowering. Then, concomitant with cotyledon  
 CC development, the level of enzyme increases with specificity for  
 CC embryonal tissues.  
 CC -!- PTM: Glycosylated.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.6e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPP 8  
 :||  
 Db 3 YPP 5

# RESULT 50

## CXAL\_CONAL

ID CXAL\_CONAL STANDARD; PRT; 16 AA.  
 AC P56639;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-conotoxin AuIA.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RA Olivera B.M., McIntosh J.M.;  
 RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic  
 RT acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A59045; A59045.  
 DR HSSP; P50984; 1PEN.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 8  
 FT DISULFID 3 16

FT MOD\_RES 16 16 AMIDATION.  
SQ SEQUENCE 16 AA; 1731 MW; 1E310FEB8FDC7001 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPP 8

:||

Db 5 YPP 7

Search completed: July 4, 2004, 04:41:31  
Job time : 6.14925 secs